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Welcome to the SIB BLAST Network Service

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NCBI BLAST program reference [PMID:9254694]:
Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query: Q9QZM7; 733 AA
Date run: 2007-11-13 20:35:31 UTC+0100 on blast01.vital-it.ch
Program: NCBI BLASTP 2.2.16 [Mar-25-2007]
Database: UniProtKB Homo sapiens
82,088 sequences; 35,064,127 total letters
UniProt Knowledgebase Release 12.4 consists of:
UniProtKB/Swiss-Prot Release 54.4 of 23-Oct-2007: 287050 entries
UniProtKB/TrEMBL Release 37.4 of 23-Oct-2007: 4988379 entries

[Taxonomic view](#) [NiceBlast view](#) [Printable view](#)

List of potentially matching sequences

Send selected sequences to ☐ Include query sequence

	Db	AC	Description	Score	E-value
<input type="checkbox"/>	tr	Q5BJG2	_HUMAN Fibroblast growth factor receptor 1 (Fms-related...	1420	0.0
<input type="checkbox"/>	sp_vs	P11362-14	Isoform 15 of P11362 - Homo sapiens (Human) [FGF...	1420	0.0
<input type="checkbox"/>	sp_vs	P11362-3	Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1...	1415	0.0
<input type="checkbox"/>	sp_vs	P11362-4	Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1...	1407	0.0
<input type="checkbox"/>	sp_vs	P11362-7	Isoform 14 of P11362 - Homo sapiens (Human) [FGFR...	1357	0.0
<input type="checkbox"/>	sp	P11362	FGFR1_HUMAN Basic fibroblast growth factor receptor 1 ...	1352	0.0
<input type="checkbox"/>	tr	Q53H63	_HUMAN Fibroblast growth factor receptor 1 isoform 2 va...	1351	0.0
<input type="checkbox"/>	tr	Q59H40	_HUMAN Fibroblast growth factor receptor 1 isoform 1 va...	1344	0.0
<input type="checkbox"/>	sp_vs	P11362-2	Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1...	1344	0.0
<input type="checkbox"/>	sp_vs	P11362-5	Isoform 10 of P11362 - Homo sapiens (Human) [FGFR...	1275	0.0
<input type="checkbox"/>	sp_vs	P11362-6	Isoform 12 of P11362 - Homo sapiens (Human) [FGFR...	1266	0.0
<input type="checkbox"/>	sp_vs	P21802-3	Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2...	1108	0.0
<input type="checkbox"/>	sp_vs	P21802-18	Isoform 18 of P21802 - Homo sapiens (Human) [FGF...	1100	0.0
<input type="checkbox"/>	sp	P21802	FGFR2_HUMAN Fibroblast growth factor receptor 2 precu...	1065	0.0
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<input type="checkbox"/>	sp_vs	P21802-4	Isoform 4 of P21802 - Homo sapiens (Human) [FGFR2...	1029	0.0
<input type="checkbox"/>	tr	Q1KHY5	_HUMAN Fibroblast growth factor receptor 2 (Bacteria-ex...	1011	0.0
<input type="checkbox"/>	sp_vs	P21802-6	Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2...	1011	0.0
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<input type="checkbox"/>	tr	Q8NI15	_HUMAN Fibroblast growth factor receptor 3 (Fragment) [...	931	0.0
<input type="checkbox"/>	tr	Q8NI16	_HUMAN Fibroblast growth factor receptor 3 (Fragment) [...	929	0.0
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<input type="checkbox"/>	tr	Q8TDA0	_HUMAN Fibroblast growth factor receptor 4 (Fibroblast ...	839	0.0
<input type="checkbox"/>	tr	Q71TW8	_HUMAN Fibroblast growth factor receptor 4, soluble-for...	805	0.0
<input type="checkbox"/>	tr	Q8IXC7	_HUMAN Isoform of FGFR2 [FGFR2 AT-I] [Homo sapiens (Hum...	770	0.0
<input type="checkbox"/>	tr	Q96KE5	_HUMAN Fibroblast growth factor receptor 4 variant [Hom...	735	0.0
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<input type="checkbox"/>	tr	Q59FL9	_HUMAN Fibroblast growth factor receptor 3 isoform 1 va...	684	0.0
<input type="checkbox"/>	tr	A8E633	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	646	0.0
<input type="checkbox"/>	tr	Q0IJ44	_HUMAN FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (...	646	0.0
<input type="checkbox"/>	sp_vs	P22607-3	Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3...	625	e-178
<input type="checkbox"/>	tr	Q59F30	_HUMAN Fibroblast growth factor receptor 4 variant (Fra...	553	e-157
<input type="checkbox"/>	tr	Q9UD50	_HUMAN Fibroblast growth factor receptor subtype 1 (Fra...	516	e-146
<input type="checkbox"/>	sp_vs	P11362-18	Isoform 18 of P11362 - Homo sapiens (Human) [FGF...	468	e-131
<input type="checkbox"/>	tr	Q53G05	_HUMAN Fibroblast growth factor receptor 1 isoform 6 va...	467	e-131
<input type="checkbox"/>	sp_vs	P11362-16	Isoform 17 of P11362 - Homo sapiens (Human) [FGF...	463	e-130
<input type="checkbox"/>	sp_vs	P21802-19	Isoform 19 of P21802 - Homo sapiens (Human) [FGF...	375	e-103
<input type="checkbox"/>	sp	P35968	VGFR2_HUMAN Vascular endothelial growth factor recepto...	325	2e-88
<input type="checkbox"/>	tr	Q59EB0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	325	2e-88
<input type="checkbox"/>	tr	A2RRS0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	325	2e-88
<input type="checkbox"/>	tr	Q2VJ45	_HUMAN HOOK3-RET fusion protein [Homo sapiens (Human)]	323	5e-88
<input type="checkbox"/>	tr	Q9BTB0	_HUMAN Ret proto-oncogene [RET] [Homo sapiens (Human)]	323	6e-88
<input type="checkbox"/>	sp	P07949	RET_HUMAN Proto-oncogene tyrosine-protein kinase recep...	323	8e-88
<input type="checkbox"/>	sp	P17948	VGFR1_HUMAN Vascular endothelial growth factor recepto...	322	1e-87
<input type="checkbox"/>	tr	Q5TAR1	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	322	1e-87
<input type="checkbox"/>	tr	Q9UMQ4	_HUMAN RET tyrosine kinase receptor (Fragment) [RET] [H...	319	1e-86
<input type="checkbox"/>	tr	Q15300	_HUMAN RET tyrosine kinase/cAMP protein kinase A subuni...	318	2e-86
<input type="checkbox"/>	tr	Q15850	_HUMAN Urf-ret protein [urf-ret] [Homo sapiens (Human)]	318	2e-86
<input type="checkbox"/>	sp	P35916	VGFR3_HUMAN Vascular endothelial growth factor recepto...	295	1e-79
<input type="checkbox"/>	tr	Q86W08	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q86W07	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	291	3e-78
<input type="checkbox"/>	tr	Q59GQ9	_HUMAN Fms-related tyrosine kinase 1 (Vascular endothel...	291	3e-78
<input type="checkbox"/>	tr	A3E342	_HUMAN IdVEGFR-1 (N2idVEGFR-1) [FLT1] [Homo sapiens (Hu...	290	8e-78
<input type="checkbox"/>	tr	Q06VW7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	277	5e-74
<input type="checkbox"/>	sp	P07333	CSF1R_HUMAN Macrophage colony-stimulating factor 1 rec...	276	9e-74
<input type="checkbox"/>	tr	Q6IQ28	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	270	6e-72
<input type="checkbox"/>	sp	P10721	KIT_HUMAN Mast/stem cell growth factor receptor precur...	266	7e-71
<input type="checkbox"/>	tr	Q99662	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	266	7e-71
<input type="checkbox"/>	sp	P35590	TIE1_HUMAN Tyrosine-protein kinase receptor Tie-1 prec...	246	1e-64
<input type="checkbox"/>	tr	Q9HBS4	_HUMAN Putative uncharacterized protein [TIE1] [Homo sa...	246	1e-64
<input type="checkbox"/>	sp	Q02763	TIE2_HUMAN Angiopoietin-1 receptor precursor (EC 2.7.1...	240	7e-63
<input type="checkbox"/>	tr	Q5TCU2	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	240	7e-63
<input type="checkbox"/>	tr	Q59HG2	_HUMAN TEK tyrosine kinase variant (Fragment) [Homo sap...	240	7e-63
<input type="checkbox"/>	tr	Q8IV34	_HUMAN TEK tyrosine kinase, endothelial (Venous malform...	239	2e-62
<input type="checkbox"/>	sp	P08069	IGF1R_HUMAN Insulin-like growth factor 1 receptor prec...	231	3e-60
<input type="checkbox"/>	sp_vs	Q16288-3	Isoform C of Q16288 - Homo sapiens (Human) [NTRK3...	225	2e-58
<input type="checkbox"/>	sp_vs	Q16288-4	Isoform D of Q16288 - Homo sapiens (Human) [NTRK3...	221	3e-57
<input type="checkbox"/>	sp	P06213	INSR_HUMAN Insulin receptor precursor (EC 2.7.10.1) (I...	218	3e-56
<input type="checkbox"/>	tr	Q59H98	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...	218	3e-56
<input type="checkbox"/>	tr	Q17RW0	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	218	3e-56
<input type="checkbox"/>	sp_vs	P06213-2	Isoform Short of P06213 - Homo sapiens (Human) [I...	218	3e-56
<input type="checkbox"/>	sp	O15146	MUSK_HUMAN Muscle, skeletal receptor tyrosine protein ...	218	4e-56
<input type="checkbox"/>	tr	Q5VZW8	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...	218	4e-56
<input type="checkbox"/>	tr	Q5VZW7	_HUMAN Muscle, skeletal, receptor tyrosine kinase [MUSK...	218	4e-56
<input type="checkbox"/>	tr	Q32MJ9	_HUMAN MUSK protein [MUSK] [Homo sapiens (Human)]	218	4e-56
<input type="checkbox"/>	tr	Q32MJ8	_HUMAN MUSK protein [MUSK] [Homo sapiens (Human)]	218	4e-56
<input type="checkbox"/>	sp	Q16288	NTRK3_HUMAN NT-3 growth factor receptor precursor (EC ...	216	1e-55
<input type="checkbox"/>	sp	P14616	INSRR_HUMAN Insulin receptor-related protein precursor...	213	9e-55
<input type="checkbox"/>	tr	Q5VZS3	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	213	9e-55

<input type="checkbox"/>	sp	Q13308	PTK7_HUMAN Tyrosine-protein kinase-like 7 precursor (C...	211	5e-54
<input type="checkbox"/>	tr	Q61Q54	_HUMAN PTK7 protein tyrosine kinase 7 [PTK7] [Homo sapi...	211	5e-54
<input type="checkbox"/>	tr	Q5T650	_HUMAN PTK7 protein tyrosine kinase 7 (PTK7 protein tyr...	211	5e-54
<input type="checkbox"/>	sp	P08922	ROS_HUMAN Proto-oncogene tyrosine-protein kinase ROS p...	210	8e-54
<input type="checkbox"/>	tr	Q5TDB4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	210	8e-54
<input type="checkbox"/>	sp	P04629	NTRK1_HUMAN High affinity nerve growth factor receptor...	209	1e-53
<input type="checkbox"/>	sp	P42679	MARK_HUMAN Megakaryocyte-associated tyrosine-protein k...	209	1e-53
<input type="checkbox"/>	tr	Q9NST8	_HUMAN Putative uncharacterized protein DKFZp434N1212 (...	209	1e-53
<input type="checkbox"/>	tr	A6NF12	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	209	1e-53
<input type="checkbox"/>	sp_vs	P04629-2	Isoform TrkA-I of P04629 - Homo sapiens (Human) [...	209	1e-53
<input type="checkbox"/>	sp	Q16620	NTRK2_HUMAN BDNF/NT-3 growth factors receptor precurs...	209	2e-53
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<input type="checkbox"/>	tr	Q8NFA8	_HUMAN Transmembrane receptor PTK7-2 (PTK7 protein tyro...	207	7e-53
<input type="checkbox"/>	sp	Q9UM73	ALK_HUMAN ALK tyrosine kinase receptor precursor (EC 2...	206	1e-52
<input type="checkbox"/>	tr	Q8TDJ5	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
<input type="checkbox"/>	tr	A6P4V4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
<input type="checkbox"/>	tr	A6P4T4	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
<input type="checkbox"/>	tr	Q8WXJ7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	206	1e-52
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<input type="checkbox"/>	sp	P42684	ABL2_HUMAN Tyrosine-protein kinase ABL2 (EC 2.7.10.2) ...	204	3e-52
<input type="checkbox"/>	tr	A0M8X0	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	204	3e-52
<input type="checkbox"/>	sp_vs	P42684-2	Isoform IA of P42684 - Homo sapiens (Human) [ABL2...	204	3e-52
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<input type="checkbox"/>	sp	P16591	FER_HUMAN Proto-oncogene tyrosine-protein kinase FER (...	204	4e-52
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<input type="checkbox"/>	tr	Q8N5L2	_HUMAN AXL receptor tyrosine kinase [AXL] [Homo sapiens...	204	6e-52
<input type="checkbox"/>	sp	P00519	ABL1_HUMAN Proto-oncogene tyrosine-protein kinase ABL1...	203	1e-51
<input type="checkbox"/>	tr	Q59FK4	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
<input type="checkbox"/>	tr	Q17R61	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
<input type="checkbox"/>	tr	A3KFPJ3	_HUMAN V-abl Abelson murine leukemia viral oncogene hom...	203	1e-51
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<input type="checkbox"/>	sp	Q12866	MERTK_HUMAN Proto-oncogene tyrosine-protein kinase MER...	201	5e-51
<input type="checkbox"/>	sp	P41240	CSK_HUMAN Tyrosine-protein kinase CSK (EC 2.7.10.2) (C...	201	5e-51
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<input type="checkbox"/>	sp	P16234	PGFRA_HUMAN Alpha-type platelet-derived growth factor ...	199	1e-50
<input type="checkbox"/>	tr	Q16176	_HUMAN Lsk protein [lsk] [Homo sapiens (Human)]	197	5e-50
<input type="checkbox"/>	tr	Q96T36	_HUMAN Fibroblast growth factor receptor 3 IIIC isoform...	196	9e-50
<input type="checkbox"/>	sp	P08631	HCK_HUMAN Tyrosine-protein kinase HCK (EC 2.7.10.2) (p...	195	3e-49
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<input type="checkbox"/>	sp	P06239	LCK_HUMAN Proto-oncogene tyrosine-protein kinase LCK (...	194	3e-49
<input type="checkbox"/>	tr	Q8N6J3	_HUMAN TYRO3 protein (Fragment) [TYRO3] [Homo sapiens (...	194	3e-49
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<input type="checkbox"/>	tr	Q59FM9	_HUMAN TYRO3 protein tyrosine kinase variant (Fragment)...	194	3e-49
<input type="checkbox"/>	sp	P34925	RYK_HUMAN Tyrosine-protein kinase RYK precursor (EC 2...	193	8e-49
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<input type="checkbox"/>	tr	Q2VXT0	_HUMAN Proto-oncogene c-fes variant 1 [Homo sapiens (Hu...	193	1e-48
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<input type="checkbox"/>	sp	P07948	LYN_HUMAN Tyrosine-protein kinase Lyn (EC 2.7.10.2) [L...	192	1e-48
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<input type="checkbox"/>	sp_vs	P07948-2	Isoform LYN B of P07948 - Homo sapiens (Human) [L...	192	1e-48
<input type="checkbox"/>	tr	Q8WTZ8	_HUMAN RYK protein (Fragment) [RYK] [Homo sapiens (Human)]	192	2e-48
<input type="checkbox"/>	sp	P09619	PGFRB_HUMAN Beta-type platelet-derived growth factor r...	191	3e-48
<input type="checkbox"/>	sp	P07332	FES_HUMAN Proto-oncogene tyrosine-protein kinase Fes/F...	191	3e-48
<input type="checkbox"/>	tr	Q59F04	_HUMAN Platelet-derived growth factor receptor beta var...	191	3e-48
<input type="checkbox"/>	sp	P36888	FLT3_HUMAN FL cytokine receptor precursor (EC 2.7.10.1...	191	5e-48
<input type="checkbox"/>	tr	Q59EB3	_HUMAN Met proto-oncogene variant (Fragment) [Homo sapi...	191	5e-48

<input type="checkbox"/>	tr	A1L467	_HUMAN Met proto-oncogene (Hepatocyte growth factor rec...	191 5e-48
<input type="checkbox"/>	sp_vs	P21802-14	Isoform 14 of P21802 - Homo sapiens (Human) [FGF...	191 5e-48
<input type="checkbox"/>	tr	Q8NFA6	_HUMAN Transmembrane receptor PTK7-4 (PTK7 protein tyro...	190 6e-48
<input type="checkbox"/>	sp	Q04912	RON_HUMAN Macrophage-stimulating protein receptor prec...	189 1e-47
<input type="checkbox"/>	sp	P08581	MET_HUMAN Hepatocyte growth factor receptor precursor ...	189 1e-47
<input type="checkbox"/>	sp	P29376	LTK_HUMAN Leukocyte tyrosine kinase receptor precursor...	189 1e-47
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<input type="checkbox"/>	sp	Q05397	FAK1_HUMAN Focal adhesion kinase 1 (EC 2.7.10.2) (FADK...	188 2e-47
<input type="checkbox"/>	tr	Q8IYN9	_HUMAN PTK2 protein [PTK2] [Homo sapiens (Human)]	188 2e-47
<input type="checkbox"/>	tr	Q658W2	_HUMAN Putative uncharacterized protein DKFZp666O0110 [...	188 2e-47
<input type="checkbox"/>	sp	Q16832	DDR2_HUMAN Discoidin domain-containing receptor 2 prec...	188 3e-47
<input type="checkbox"/>	sp	Q01973	ROR1_HUMAN Tyrosine-protein kinase transmembrane recep...	187 4e-47
<input type="checkbox"/>	tr	Q72730	_HUMAN Discoidin domain receptor family, member 2 (Disc...	187 4e-47
<input type="checkbox"/>	tr	A2VCQ3	_HUMAN ROR1 protein (Fragment) [ROR1] [Homo sapiens (Hu...	187 4e-47
<input type="checkbox"/>	tr	Q6MZT2	_HUMAN Putative uncharacterized protein DKFZp686D1354 [...	187 5e-47
<input type="checkbox"/>	tr	Q8N9D7	_HUMAN CDNA FLJ37680 fis, clone BRHIP2012923, highly si...	186 9e-47
<input type="checkbox"/>	tr	Q59GN8	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186 9e-47
<input type="checkbox"/>	tr	Q59GM6	_HUMAN PTK2 protein tyrosine kinase 2 isoform b variant...	186 9e-47
<input type="checkbox"/>	tr	Q12787	_HUMAN Receptor tyrosine kinase (Fragment) [Homo sapien...	186 9e-47
<input type="checkbox"/>	tr	Q5VTU6	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) [...	185 2e-46
<input type="checkbox"/>	sp	Q13882	PTK6_HUMAN Tyrosine-protein kinase 6 (EC 2.7.10.2) (Br...	184 6e-46
<input type="checkbox"/>	sp	Q01974	ROR2_HUMAN Tyrosine-protein kinase transmembrane recep...	183 8e-46
<input type="checkbox"/>	tr	Q5VTT3	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183 8e-46
<input type="checkbox"/>	tr	A6NNI9	_HUMAN Uncharacterized protein ROR2 [ROR2] [Homo sapien...	183 8e-46
<input type="checkbox"/>	tr	A1L4F5	_HUMAN Receptor tyrosine kinase-like orphan receptor 2 ...	183 8e-46
<input type="checkbox"/>	sp_vs	P06239-3	Isoform 3 of P06239 - Homo sapiens (Human) [LCK] ...	183 8e-46
<input type="checkbox"/>	sp	P12931	SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src (...	182 2e-45
<input type="checkbox"/>	sp	P51813	BMX_HUMAN Cytoplasmic tyrosine-protein kinase BMX (EC ...	182 2e-45
<input type="checkbox"/>	tr	Q76P87	_HUMAN V-src sarcoma (Schmidt-Ruppin A-2) viral oncogen...	182 2e-45
<input type="checkbox"/>	sp_vs	P12931-2	Isoform 2 of P12931 - Homo sapiens (Human) [SRC] ...	182 2e-45
<input type="checkbox"/>	sp	P51451	BLK_HUMAN Tyrosine-protein kinase BLK (EC 2.7.10.2) (B...	182 2e-45
<input type="checkbox"/>	tr	Q96IN1	_HUMAN B lymphoid tyrosine kinase (B lymphoid tyrosine ...	182 2e-45
<input type="checkbox"/>	tr	Q96T35	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	181 5e-45
<input type="checkbox"/>	tr	Q5R3A8	_HUMAN FYN oncogene related to SRC, FGR, YES [FYN] [Hom...	181 5e-45
<input type="checkbox"/>	tr	A6NIP9	_HUMAN Uncharacterized protein FYN [FYN] [Homo sapiens ...	181 5e-45
<input type="checkbox"/>	tr	Q6NSK4	_HUMAN DDR1 protein [DDR1] [Homo sapiens (Human)]	180 7e-45
<input type="checkbox"/>	tr	A6NP30	_HUMAN Uncharacterized protein PTK7 [PTK7] [Homo sapien...	180 9e-45
<input type="checkbox"/>	sp_vs	P06241-2	Isoform 2 of P06241 - Homo sapiens (Human) [FYN] ...	180 9e-45
<input type="checkbox"/>	sp	Q08345	DDR1_HUMAN Epithelial discoidin domain-containing rece...	179 1e-44
<input type="checkbox"/>	tr	Q5ST11	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179 1e-44
<input type="checkbox"/>	tr	Q573B4	_HUMAN Proto-oncogene tyrosine-protein kinase LCK [LCK]...	179 1e-44
<input type="checkbox"/>	tr	Q4LE50	_HUMAN DDR1 variant protein (Fragment) [DDR1 variant pr...	179 1e-44
<input type="checkbox"/>	tr	Q2L6H3	_HUMAN Discoidin domain receptor family, member 1 (Disc...	179 1e-44
<input type="checkbox"/>	sp_vs	Q08345-2	Isoform 2 of Q08345 - Homo sapiens (Human) [DDR1]...	179 1e-44
<input type="checkbox"/>	sp	P07947	YES_HUMAN Proto-oncogene tyrosine-protein kinase Yes (...	179 1e-44
<input type="checkbox"/>	sp	P42680	TEC_HUMAN Tyrosine-protein kinase Tec (EC 2.7.10.2) [T...	178 3e-44
<input type="checkbox"/>	tr	A6NIH9	_HUMAN Uncharacterized protein BMX [BMX] [Homo sapiens ...	178 3e-44
<input type="checkbox"/>	sp	Q15375	EPHA7_HUMAN Ephrin type-A receptor 7 precursor (EC 2.7...	177 4e-44
<input type="checkbox"/>	tr	A6NLB3	_HUMAN Uncharacterized protein YES1 [YES1] [Homo sapien...	177 4e-44
<input type="checkbox"/>	sp_vs	Q15375-2	Isoform 2 of Q15375 - Homo sapiens (Human) [EPHA7...	177 4e-44
<input type="checkbox"/>	sp	P06241	FYN_HUMAN Proto-oncogene tyrosine-protein kinase Fyn (...	176 1e-43
<input type="checkbox"/>	sp	Q14289	FAK2_HUMAN Protein tyrosine kinase 2 beta (EC 2.7.10.2...	176 1e-43
<input type="checkbox"/>	sp	P29320	EPHA3_HUMAN Ephrin type-A receptor 3 precursor (EC 2.7...	176 1e-43
<input type="checkbox"/>	tr	Q6ZRA8	_HUMAN CDNA FLJ46514 fis, clone THYMU3032798, highly si...	176 1e-43
<input type="checkbox"/>	tr	Q6PID4	_HUMAN PTK2B protein tyrosine kinase 2 beta [PTK2B] [Ho...	176 1e-43
<input type="checkbox"/>	tr	Q6P4R6	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA3] [Homo sapi...	176 1e-43
<input type="checkbox"/>	tr	Q59GM4	_HUMAN PTK2B protein tyrosine kinase 2 beta isoform a v...	176 1e-43
<input type="checkbox"/>	sp_vs	Q14289-2	Isoform 2 of Q14289 - Homo sapiens (Human) [PTK2B...	176 1e-43
<input type="checkbox"/>	sp_vs	Q05397-2	Isoform 2 of Q05397 - Homo sapiens (Human) [PTK2]...	176 1e-43
<input type="checkbox"/>	sp	P04626	ERBB2_HUMAN Receptor tyrosine-protein kinase erbB-2 pr...	176 2e-43
<input type="checkbox"/>	tr	Q05D26	_HUMAN BLK protein (Fragment) [BLK] [Homo sapiens (Human)]	176 2e-43
<input type="checkbox"/>	sp	P09769	FGR_HUMAN Proto-oncogene tyrosine-protein kinase FGR (...	175 2e-43
<input type="checkbox"/>	sp	Q15303	ERBB4_HUMAN Receptor tyrosine-protein kinase erbB-4 pr...	175 2e-43
<input type="checkbox"/>	sp_vs	Q15303-2	Isoform JM-B of Q15303 - Homo sapiens (Human) [ER...	175 2e-43

<input type="checkbox"/>	sp_vs	Q15303-3	Isoform 3 of Q15303 - Homo sapiens (Human) [ERBB4...	175	2e-43
<input type="checkbox"/>	sp	P29322	EPHA8_HUMAN Ephrin type-A receptor 8 precursor (EC 2.7...	175	3e-43
<input type="checkbox"/>	sp_vs	Q05397-3	Isoform 3 of Q05397 - Homo sapiens (Human) [PTK2]...	174	5e-43
<input type="checkbox"/>	sp	P54756	EPHA5_HUMAN Ephrin type-A receptor 5 precursor (EC 2.7...	174	6e-43
<input type="checkbox"/>	sp	P29317	EPHA2_HUMAN Ephrin type-A receptor 2 precursor (EC 2.7...	174	6e-43
<input type="checkbox"/>	tr	Q8N3Z2	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA2] [Homo sapi...	174	6e-43
<input type="checkbox"/>	tr	Q59FT4	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...	174	6e-43
<input type="checkbox"/>	tr	A2ARL4	_HUMAN Discoidin domain receptor family, member 1 (Frag...	174	6e-43
<input type="checkbox"/>	sp_vs	P54756-2	Isoform 2 of P54756 - Homo sapiens (Human) [EPHA5...	174	6e-43
<input type="checkbox"/>	sp	P54764	EPHA4_HUMAN Ephrin type-A receptor 4 precursor (EC 2.7...	171	3e-42
<input type="checkbox"/>	sp	P21709	EPHA1_HUMAN Ephrin type-A receptor 1 precursor (EC 2.7...	171	3e-42
<input type="checkbox"/>	tr	Q58F15	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA4] [Homo sapi...	171	3e-42
<input type="checkbox"/>	tr	Q53TA0	_HUMAN Putative uncharacterized protein EPHA4 (Fragment...	171	3e-42
<input type="checkbox"/>	tr	A1L3V3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHA1] [Homo sapi...	171	3e-42
<input type="checkbox"/>	tr	Q9NSQ6	_HUMAN Putative uncharacterized protein DKFZp434L0319 (...	171	5e-42
<input type="checkbox"/>	tr	Q7Z3F2	_HUMAN Ephrin receptor (EC 2.7.10.1) [DKFZp686C0686] [H...	171	5e-42
<input type="checkbox"/>	sp	P29323	EPHB2_HUMAN Ephrin type-B receptor 2 precursor (EC 2.7...	169	2e-41
<input type="checkbox"/>	tr	Q5TFU3	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...	169	2e-41
<input type="checkbox"/>	tr	Q4LE53	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [EPHB2 ...	169	2e-41
<input type="checkbox"/>	tr	A6NJM0	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB2] [Homo sapi...	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-2	Isoform 2 of P29323 - Homo sapiens (Human) [EPHB2...	169	2e-41
<input type="checkbox"/>	sp_vs	P29323-3	Isoform 3 of P29323 - Homo sapiens (Human) [EPHB2...	169	2e-41
<input type="checkbox"/>	sp	Q06187	BTX_HUMAN Tyrosine-protein kinase BTK (EC 2.7.10.2) (B...	169	2e-41
<input type="checkbox"/>	sp	P00533	EGFR_HUMAN Epidermal growth factor receptor precursor ...	168	3e-41
<input type="checkbox"/>	tr	Q59FL8	_HUMAN Epidermal growth factor receptor isoform a varia...	168	3e-41
<input type="checkbox"/>	tr	Q504U8	_HUMAN EGFR protein [EGFR] [Homo sapiens (Human)]	168	3e-41
<input type="checkbox"/>	tr	Q2TTR7	_HUMAN Cell growth inhibiting protein 40 [Homo sapiens ...	168	3e-41
<input type="checkbox"/>	tr	Q4JFK8	_HUMAN Fes/fps proto-oncogene (Fragment) [FES] [Homo sa...	168	3e-41
<input type="checkbox"/>	tr	Q59CQ2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) (Fragment)...	167	4e-41
<input type="checkbox"/>	sp	P42681	TXK_HUMAN Tyrosine-protein kinase TXK (EC 2.7.10.2) [T...	167	6e-41
<input type="checkbox"/>	sp	O60674	JAK2_HUMAN Tyrosine-protein kinase JAK2 (EC 2.7.10.2) ...	166	1e-40
<input type="checkbox"/>	tr	Q8IXP2	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...	166	1e-40
<input type="checkbox"/>	tr	Q506Q0	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK2] [Ho...	166	1e-40
<input type="checkbox"/>	sp	P54762	EPHB1_HUMAN Ephrin type-B receptor 1 precursor (EC 2.7...	166	1e-40
<input type="checkbox"/>	sp_vs	P54762-2	Isoform 2 of P54762 - Homo sapiens (Human) [EPHB1...	166	1e-40
<input type="checkbox"/>	tr	Q0VG87	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB1] [Homo sapi...	165	3e-40
<input type="checkbox"/>	sp	P23458	JAK1_HUMAN Tyrosine-protein kinase JAK1 (EC 2.7.10.2) ...	164	4e-40
<input type="checkbox"/>	sp	P43405	KSYK_HUMAN Tyrosine-protein kinase SYK (EC 2.7.10.2) (...	164	6e-40
<input type="checkbox"/>	tr	Q5T6N8	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...	164	6e-40
<input type="checkbox"/>	tr	Q5T6N7	_HUMAN Spleen tyrosine kinase (Spleen tyrosine kinase, ...	164	6e-40
<input type="checkbox"/>	tr	Q59FQ5	_HUMAN RYK receptor-like tyrosine kinase isoform 1 vari...	164	6e-40
<input type="checkbox"/>	sp_vs	P43405-2	Isoform Short of P43405 - Homo sapiens (Human) [S...	164	6e-40
<input type="checkbox"/>	sp	P54760	EPHB4_HUMAN Ephrin type-B receptor 4 precursor (EC 2.7...	163	8e-40
<input type="checkbox"/>	tr	Q96L35	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	tr	Q7Z635	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	tr	Q59F17	_HUMAN Ephrin receptor (EC 2.7.10.1) (Fragment) [Homo s...	163	8e-40
<input type="checkbox"/>	tr	Q541P7	_HUMAN Ephrin receptor (EC 2.7.10.1) [EPHB4] [Homo sapi...	163	8e-40
<input type="checkbox"/>	sp	Q08881	ITK_HUMAN Tyrosine-protein kinase ITK/TSK (EC 2.7.10.2...	163	1e-39
<input type="checkbox"/>	tr	Q9UMB0	_HUMAN Fibroblast growth factor receptor-related protei...	162	1e-39
<input type="checkbox"/>	tr	Q9H7V3	_HUMAN CDNA FLJ14219 fis, clone NT2RP3003800, highly si...	162	2e-39
<input type="checkbox"/>	sp	P43403	ZAP70_HUMAN Tyrosine-protein kinase ZAP-70 (EC 2.7.10....	160	5e-39
<input type="checkbox"/>	tr	Q6PIA4	_HUMAN ZAP70 protein (Putative uncharacterized protein ...	160	5e-39
<input type="checkbox"/>	sp	P54753	EPHB3_HUMAN Ephrin type-B receptor 3 precursor (EC 2.7...	160	7e-39
<input type="checkbox"/>	sp_vs	P06241-3	Isoform 3 of P06241 - Homo sapiens (Human) [FYN] ...	160	9e-39
<input type="checkbox"/>	sp_vs	Q01973-2	Isoform Short of Q01973 - Homo sapiens (Human) [R...	160	9e-39
<input type="checkbox"/>	sp	Q6J9G0	STYK1_HUMAN Tyrosine protein-kinase STYK1 (EC 2.7.10.2...	158	4e-38
<input type="checkbox"/>	sp	Q07912	ACK1_HUMAN Activated CDC42 kinase 1 (EC 2.7.10.2) (ACK...	156	1e-37
<input type="checkbox"/>	tr	Q6ZMQ0	_HUMAN CDNA FLJ16772 fis, clone BRAWH3043827, highly si...	156	1e-37
<input type="checkbox"/>	sp_vs	Q07912-2	Isoform 2 of Q07912 - Homo sapiens (Human) [TNK2]...	156	1e-37
<input type="checkbox"/>	sp	P29597	TYK2_HUMAN Non-receptor tyrosine-protein kinase TYK2 (...	155	2e-37
<input type="checkbox"/>	tr	Q2VKS9	_HUMAN Proto-oncogene c-fes variant 2 [Homo sapiens (Hu...	155	2e-37
<input type="checkbox"/>	tr	Q8IXD6	_HUMAN Truncated ZAP kinase [Homo sapiens (Human)]	155	2e-37
<input type="checkbox"/>	tr	Q6LBK2	_HUMAN Acidic fibroblast growth factor (Fragment) [FGFR...	155	2e-37
<input type="checkbox"/>	tr	Q4LDX3	_HUMAN Janus kinase 1 [JAK1] [Homo sapiens (Human)]	154	5e-37
<input type="checkbox"/>	tr	Q96T34	_HUMAN Fibroblast growth factor receptor 3 IIIc isoform...	154	7e-37
<input type="checkbox"/>	tr	A6NFP4	_HUMAN Uncharacterized protein ZAP70 [ZAP70] [Homo sapi...	154	7e-37

<input type="checkbox"/>	tr	Q53T57	_HUMAN Putative uncharacterized protein ERBB4 (Fragment...	152	2e-36
<input type="checkbox"/>	sp	P52333	JAK3_HUMAN Tyrosine-protein kinase JAK3 (EC 2.7.10.2) ...	152	3e-36
<input type="checkbox"/>	tr	Q99699	_HUMAN Tyrosine-protein kinase (EC 2.7.10.2) [JAK3] [Ho...	152	3e-36
<input type="checkbox"/>	tr	Q75MF2	_HUMAN Putative uncharacterized protein EGFR (Fragment)...	150	1e-35
<input type="checkbox"/>	tr	Q59FX1	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	150	1e-35
<input type="checkbox"/>	sp	P21860	ERBB3_HUMAN Receptor tyrosine-protein kinase erbB-3 pr...	148	4e-35
<input type="checkbox"/>	tr	Q15516	_HUMAN Tyrosine kinase [Homo sapiens (Human)]	147	6e-35
<input type="checkbox"/>	sp	Q5JZY3	EPHAA_HUMAN Ephrin type-A receptor 10 precursor (EC 2...	145	2e-34
<input type="checkbox"/>	tr	Q3MS96	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	145	2e-34
<input type="checkbox"/>	sp	Q9UF33	EPHA6_HUMAN Ephrin type-A receptor 6 precursor (EC 2.7...	144	7e-34
<input type="checkbox"/>	tr	Q6ZNH1	_HUMAN CDNA FLJ16103 fis, clone TESTI2016663, moderatel...	144	7e-34
<input type="checkbox"/>	sp_vs	P54762-3	Isoform 3 of P54762 - Homo sapiens (Human) [EPHB1...	142	3e-33
<input type="checkbox"/>	tr	Q96HF4	_HUMAN EPHA2 protein (Fragment) [EPHA2] [Homo sapiens (...]	141	3e-33
<input type="checkbox"/>	sp	Q96Q04	LMTK3_HUMAN Serine/threonine-protein kinase LMTK3 prec...	135	2e-31
<input type="checkbox"/>	sp	Q12852	M3K12_HUMAN Mitogen-activated protein kinase kinase ki...	134	5e-31
<input type="checkbox"/>	sp	Q8N441	FGRL1_HUMAN Fibroblast growth factor receptor-like 1 p...	133	9e-31
<input type="checkbox"/>	tr	Q9P0L3	_HUMAN Bruton's tyrosine kinase (Fragment) [Homo sapien...	133	9e-31
<input type="checkbox"/>	tr	Q6ZMD4	_HUMAN CDNA FLJ23990 fis, clone HRC08053, highly simila...	133	9e-31
<input type="checkbox"/>	tr	A4FU89	_HUMAN EPHA10 protein [EPHA10] [Homo sapiens (Human)]	132	2e-30
<input type="checkbox"/>	sp_vs	Q5JZY3-3	Isoform 3 of Q5JZY3 - Homo sapiens (Human) [EPHA1...	132	2e-30
<input type="checkbox"/>	tr	Q3MS92	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	132	3e-30
<input type="checkbox"/>	tr	Q9P0L5	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	131	5e-30
<input type="checkbox"/>	sp_vs	P52333-2	Isoform 1 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
<input type="checkbox"/>	sp_vs	P52333-3	Isoform 3 of P52333 - Homo sapiens (Human) [JAK3]...	131	5e-30
<input type="checkbox"/>	sp	Q13470	TNK1_HUMAN Non-receptor tyrosine-protein kinase TNK1 (...]	130	8e-30
<input type="checkbox"/>	tr	Q9P0L7	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
<input type="checkbox"/>	tr	Q9P0L6	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	8e-30
<input type="checkbox"/>	sp_vs	Q13470-2	Isoform 2 of Q13470 - Homo sapiens (Human) [TNK1]...	130	8e-30
<input type="checkbox"/>	tr	Q9NPI3	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
<input type="checkbox"/>	tr	Q9NPI2	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	130	1e-29
<input type="checkbox"/>	sp	Q9NYL2	MLTK_HUMAN Mitogen-activated protein kinase kinase kin...	129	2e-29
<input type="checkbox"/>	sp	O43283	M3K13_HUMAN Mitogen-activated protein kinase kinase ki...	129	2e-29
<input type="checkbox"/>	sp_vs	Q9NYL2-2	Isoform 2 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
<input type="checkbox"/>	sp_vs	Q9NYL2-3	Isoform 3 of Q9NYL2 - Homo sapiens (Human) [MLTK]...	129	2e-29
<input type="checkbox"/>	tr	Q59GJ7	_HUMAN Tyrosine-protein kinase receptor (EC 2.7.10.1) (...]	129	2e-29
<input type="checkbox"/>	sp	Q02779	M3K10_HUMAN Mitogen-activated protein kinase kinase ki...	128	4e-29
<input type="checkbox"/>	sp	P80192	M3K9_HUMAN Mitogen-activated protein kinase kinase kin...	127	5e-29
<input type="checkbox"/>	tr	A3KN85	_HUMAN MAP3K9 protein [MAP3K9] [Homo sapiens (Human)]	127	5e-29
<input type="checkbox"/>	sp_vs	P80192-4	Isoform 2 of P80192 - Homo sapiens (Human) [MAP3K...	127	5e-29
<input type="checkbox"/>	sp	Q6ZMQ8	LMTK1_HUMAN Serine/threonine-protein kinase LMTK1 (EC ...]	124	4e-28
<input type="checkbox"/>	tr	Q6P4H5	_HUMAN PDGFRA protein [PDGFRA] [Homo sapiens (Human)]	124	4e-28
<input type="checkbox"/>	sp_vs	Q6ZMQ8-3	Isoform 3 of Q6ZMQ8 - Homo sapiens (Human) [AATK]...	124	4e-28
<input type="checkbox"/>	sp	Q5TCX8	M3KL4_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
<input type="checkbox"/>	sp	Q16584	M3K11_HUMAN Mitogen-activated protein kinase kinase ki...	123	1e-27
<input type="checkbox"/>	sp_vs	Q5TCX8-2	Isoform 2 of Q5TCX8 - Homo sapiens (Human) [MLK4]...	123	1e-27
<input type="checkbox"/>	sp	Q15197	EPHB6_HUMAN Ephrin type-B receptor 6 precursor (Tyrosi...	122	2e-27
<input type="checkbox"/>	tr	Q2TB24	_HUMAN EPHB6 protein (EPH receptor B6, isoform CRA_b) [...]	122	2e-27
<input type="checkbox"/>	tr	Q2TB23	_HUMAN EPH receptor B6 (EphB6) [EPHB6] [Homo sapiens (H...	122	2e-27
<input type="checkbox"/>	tr	Q9UMA9	_HUMAN Fibroblast growth factor receptor (Fragment) [BE...	122	3e-27
<input type="checkbox"/>	tr	Q9P0M0	_HUMAN Bruton's tyrosine kinase [Homo sapiens (Human)]	121	4e-27
<input type="checkbox"/>	sp	O43318	M3K7_HUMAN Mitogen-activated protein kinase kinase kin...	113	1e-24
<input type="checkbox"/>	tr	Q9NZ70	_HUMAN TGF beta-activated kinase splice variant d (Mito...	113	1e-24
<input type="checkbox"/>	tr	Q5U0D0	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
<input type="checkbox"/>	tr	Q5TDM9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	113	1e-24
<input type="checkbox"/>	sp_vs	O43318-2	Isoform 1A of O43318 - Homo sapiens (Human) [MAP3...	113	1e-24
<input type="checkbox"/>	sp_vs	O43318-3	Isoform 1C of O43318 - Homo sapiens (Human) [MAP3...	113	1e-24
<input type="checkbox"/>	tr	Q5U0C9	_HUMAN Mitogen-activated protein kinase kinase kinase 7...	112	2e-24
<input type="checkbox"/>	tr	Q5JY90	_HUMAN Bruton agammaglobulinemia tyrosine kinase (Bruto...	110	8e-24
<input type="checkbox"/>	sp	P04049	RAF1_HUMAN RAF proto-oncogene serine/threonine-protein...	104	5e-22
<input type="checkbox"/>	tr	Q59HE0	_HUMAN Colony stimulating factor 1 receptor variant (Fr...	104	5e-22
<input type="checkbox"/>	tr	Q15278	_HUMAN RAF1 protein (Fragment) [RAF1] [Homo sapiens (Hu...	104	5e-22
<input type="checkbox"/>	sp	Q13546	RIPK1_HUMAN Receptor-interacting serine/threonine-prot...	103	8e-22
<input type="checkbox"/>	sp	Q8IWU2	LMTK2_HUMAN Serine/threonine-protein kinase LMTK2 prec...	103	1e-21
<input type="checkbox"/>	tr	A4D272	_HUMAN Lemur tyrosine kinase 2 (Lemur tyrosine kinase 2...	103	1e-21
<input type="checkbox"/>	sp	P15056	BRAF1_HUMAN B-Raf proto-oncogene serine/threonine-prot...	102	2e-21
<input type="checkbox"/>	tr	Q5IBP5	_HUMAN AKAP9-BRAF fusion protein [Homo sapiens (Human)]	102	2e-21

<input type="checkbox"/>	tr	A4D1T4	_HUMAN V-raf murine sarcoma viral oncogene homolog B1 [...	102	2e-21
<input type="checkbox"/>	tr	Q5UBV6	_HUMAN NIN/PDGFRB fusion protein (Fragment) [NIN/PDGFRB...	102	3e-21
<input type="checkbox"/>	sp	P53667	LIMK1_HUMAN LIM domain kinase 1 (EC 2.7.11.1) (LIMK-1)...	101	5e-21
<input type="checkbox"/>	sp_vs	P53667-2	Isoform 2 of P53667 - Homo sapiens (Human) [LIMK1...	101	5e-21
<input type="checkbox"/>	sp	P10398	ARAF_HUMAN A-Raf proto-oncogene serine/threonine-prote...	100	7e-21
<input type="checkbox"/>	tr	Q96II5	_HUMAN ARAF protein [ARAF] [Homo sapiens (Human)]	100	7e-21
<input type="checkbox"/>	tr	Q8TCG9	_HUMAN KIT protein (Fragment) [KIT] [Homo sapiens (Human)]	100	9e-21
<input type="checkbox"/>	sp	Q96S53	TESK2_HUMAN Dual specificity testis-specific protein k...	99	2e-20
<input type="checkbox"/>	tr	Q5T152	_HUMAN Testis-specific kinase 2 (Testis-specific kinase...	99	2e-20
<input type="checkbox"/>	sp	Q9Y6E0	STK24_HUMAN Serine/threonine-protein kinase 24 (EC 2.7...	99	3e-20
<input type="checkbox"/>	tr	Q6P0Y1	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	Q5U0E6	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	Q5T5B3	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	99	3e-20
<input type="checkbox"/>	tr	A0PJ49	_HUMAN FGFR1 protein (Fragment) [FGFR1] [Homo sapiens...	99	3e-20
<input type="checkbox"/>	sp_vs	Q9Y6E0-2	Isoform A of Q9Y6E0 - Homo sapiens (Human) [STK24...	99	3e-20
<input type="checkbox"/>	sp	Q04759	KPCT_HUMAN Protein kinase C theta type (EC 2.7.11.13) ...	98	4e-20
<input type="checkbox"/>	tr	Q9UDF1	_HUMAN Fibroblast growth factor receptor 1 THIRD immuno...	98	4e-20
<input type="checkbox"/>	tr	Q5JUN8	_HUMAN Protein kinase C, theta (Fragment) [PRKCQ] [Homo...	98	4e-20
<input type="checkbox"/>	sp	Q6P3R8	NEK5_HUMAN Serine/threonine-protein kinase Nek5 (EC 2....	97	1e-19
<input type="checkbox"/>	tr	Q6PG81	_HUMAN STK24 protein (Fragment) [STK24] [Homo sapiens (...	97	1e-19
<input type="checkbox"/>	tr	A6NIT1	_HUMAN Uncharacterized protein ARAF [ARAF] [Homo sapien...	96	2e-19
<input type="checkbox"/>	sp	Q15416	KS6A1_HUMAN Ribosomal protein S6 kinase alpha-1 (EC 2....	95	4e-19
<input type="checkbox"/>	tr	A6NGG4	_HUMAN Uncharacterized protein RPS6KA1 [RPS6KA1] [Homo ...	95	4e-19
<input type="checkbox"/>	tr	A6NFC2	_HUMAN Uncharacterized protein ERBB2 [ERBB2] [Homo sapi...	95	5e-19
<input type="checkbox"/>	sp	Q9H2G2	SLK_HUMAN STE20-like serine/threonine-protein kinase (...	94	8e-19
<input type="checkbox"/>	sp	Q9P0L2	MARK1_HUMAN Serine/threonine-protein kinase MARK1 (EC ...	94	8e-19
<input type="checkbox"/>	sp_vs	Q9H2G2-2	Isoform 2 of Q9H2G2 - Homo sapiens (Human) [SLK] ...	94	8e-19
<input type="checkbox"/>	sp_vs	P27448-3	Isoform 3 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-4	Isoform 4 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-5	Isoform 5 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	sp_vs	P27448-6	Isoform 6 of P27448 - Homo sapiens (Human) [MARK3...	94	1e-18
<input type="checkbox"/>	tr	Q14219	_HUMAN Protein tyrosine kinase (Fragment) [tec] [Homo s...	93	1e-18
<input type="checkbox"/>	sp	Q7KZI7	MARK2_HUMAN Serine/threonine-protein kinase MARK2 (EC ...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-2	Isoform 2 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-3	Isoform 3 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-4	Isoform 4 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-5	Isoform 5 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-6	Isoform 6 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-7	Isoform 7 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-8	Isoform 8 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-9	Isoform 9 of Q7KZI7 - Homo sapiens (Human) [MARK2...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-10	Isoform 10 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-11	Isoform 11 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp_vs	Q7KZI7-12	Isoform 12 of Q7KZI7 - Homo sapiens (Human) [MAR...	93	2e-18
<input type="checkbox"/>	sp	Q15569	TESK1_HUMAN Dual specificity testis-specific protein k...	92	3e-18
<input type="checkbox"/>	tr	Q8IXZ8	_HUMAN TESK1 protein (Testis-specific kinase 1, isoform...	92	3e-18
<input type="checkbox"/>	tr	Q59FZ4	_HUMAN Serine/threonine kinase 4 variant (Fragment) [Ho...	92	3e-18
<input type="checkbox"/>	sp	Q8TDX7	NEK7_HUMAN Serine/threonine-protein kinase Nek7 (EC 2....	91	5e-18
<input type="checkbox"/>	sp	P05771	KPCB_HUMAN Protein kinase C beta type (EC 2.7.11.13) (...	91	5e-18
<input type="checkbox"/>	tr	A6NH24	_HUMAN Uncharacterized protein ROBO1 [ROBO1] [Homo sapi...	91	5e-18
<input type="checkbox"/>	sp_vs	P05771-2	Isoform Beta-II of P05771 - Homo sapiens (Human) ...	91	5e-18
<input type="checkbox"/>	sp	Q15349	KS6A2_HUMAN Ribosomal protein S6 kinase alpha-2 (EC 2....	91	7e-18
<input type="checkbox"/>	tr	Q05DF6	_HUMAN NEK4 protein (Fragment) [NEK4] [Homo sapiens (Hu...	91	7e-18
<input type="checkbox"/>	tr	A6NND1	_HUMAN Uncharacterized protein RPS6KA2 [RPS6KA2] [Homo ...	91	7e-18
<input type="checkbox"/>	sp_vs	Q05397-4	Isoform 4 of Q05397 - Homo sapiens (Human) [PTK2]...	91	7e-18
<input type="checkbox"/>	sp_vs	Q15349-2	Isoform 2 of Q15349 - Homo sapiens (Human) [RPS6K...	91	7e-18
<input type="checkbox"/>	sp	Q9Y6N7	ROBO1_HUMAN Roundabout homolog 1 precursor (H-Robo-1) ...	91	9e-18
<input type="checkbox"/>	sp	P51957	NEK4_HUMAN Serine/threonine-protein kinase Nek4 (EC 2....	91	9e-18
<input type="checkbox"/>	sp	P51812	KS6A3_HUMAN Ribosomal protein S6 kinase alpha-3 (EC 2....	91	9e-18
<input type="checkbox"/>	tr	Q6P576	_HUMAN NEK4 protein [Homo sapiens (Human)]	91	9e-18
<input type="checkbox"/>	sp_vs	Q9Y6N7-2	Isoform 2 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...	91	9e-18
<input type="checkbox"/>	sp	Q9UEW8	STK39_HUMAN STE20/SPS1-related proline-alanine-rich pr...	90	1e-17
<input type="checkbox"/>	tr	Q53S90	_HUMAN Putative uncharacterized protein STK39 (Fragment...	90	1e-17
<input type="checkbox"/>	sp	P27448	MARK3_HUMAN MAP/microtubule affinity-regulating kinase...	90	2e-17
<input type="checkbox"/>	sp_vs	P27448-2	Isoform 2 of P27448 - Homo sapiens (Human) [MARK3...	90	2e-17
<input type="checkbox"/>	sp_vs	P27448-7	Isoform 7 of P27448 - Homo sapiens (Human) [MARK3...	90	2e-17

<input type="checkbox"/>	tr	Q8NFEJ4	_HUMAN Testis-specific kinase-1 (Fragment) [Homo sapien...	89 2e-17
<input type="checkbox"/>	tr	Q6NSK0	_HUMAN Serine/threonine kinase 10 [STK10] [Homo sapiens...	89 2e-17
<input type="checkbox"/>	tr	Q2M1J3	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	tr	Q1RMC8	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	tr	Q1RMC7	_HUMAN ROBO1 protein [ROBO1] [Homo sapiens (Human)]	89 2e-17
<input type="checkbox"/>	sp_vs	Q9Y6N7-3	Isoform 3 of Q9Y6N7 - Homo sapiens (Human) [ROBO1...	89 2e-17
<input type="checkbox"/>	sp	Q9H0K1	SN1L2_HUMAN Serine/threonine-protein kinase SNF1-like ...	89 3e-17
<input type="checkbox"/>	sp	Q9H093	NUAK2_HUMAN NUA family SNF1-like kinase 2 (EC 2.7.11....	89 3e-17
<input type="checkbox"/>	sp	Q9P289	MST4_HUMAN Serine/threonine-protein kinase MST4 (EC 2....	89 3e-17
<input type="checkbox"/>	tr	Q8NBY1	_HUMAN CDNA FLJ90669 fis, clone PLACE1005519, moderatel...	89 3e-17
<input type="checkbox"/>	tr	Q499L9	_HUMAN Serine/threonine protein kinase MST4 [MST4] [Hom...	89 3e-17
<input type="checkbox"/>	sp	Q9NRP7	STK36_HUMAN Serine/threonine-protein kinase 36 (EC 2.7...	89 3e-17
<input type="checkbox"/>	sp	P51956	NEK3_HUMAN Serine/threonine-protein kinase Nek3 (EC 2....	89 3e-17
<input type="checkbox"/>	tr	Q6ZN64	_HUMAN CDNA FLJ16392 fis, clone TRACH2020048, moderatel...	89 3e-17
<input type="checkbox"/>	tr	Q5TAP2	_HUMAN NIMA (Never in mitosis gene a)-related kinase 3 ...	89 3e-17
<input type="checkbox"/>	tr	Q5T153	_HUMAN Testis-specific kinase 2 [TESK2] [Homo sapiens (...	89 3e-17
<input type="checkbox"/>	tr	P78483	_HUMAN C-src-2 protein (Fragment) [FGR] [Homo sapiens (...	89 3e-17
<input type="checkbox"/>	tr	A5YM70	_HUMAN NEK4 protein [NEK4] [Homo sapiens (Human)]	89 3e-17
<input type="checkbox"/>	sp_vs	Q9NRP7-2	Isoform 2 of Q9NRP7 - Homo sapiens (Human) [STK36...	89 3e-17
<input type="checkbox"/>	sp_vs	Q96S53-3	Isoform 3 of Q96S53 - Homo sapiens (Human) [TESK2...	89 3e-17
<input type="checkbox"/>	tr	Q9UEH2	_HUMAN BEK fibroblast growth factor receptor (Fragment)...	88 4e-17
<input type="checkbox"/>	tr	Q8J023	_HUMAN NIMA-related protein kinase 3 [NEK3] [Homo sapie...	88 4e-17
<input type="checkbox"/>	tr	Q572P5	_HUMAN Tyrosine-protein kinase BTK isoform 65 (Fragment...	88 4e-17
<input type="checkbox"/>	tr	Q08AP4	_HUMAN PKN2 protein [PKN2] [Homo sapiens (Human)]	88 4e-17
<input type="checkbox"/>	sp	Q13043	STK4_HUMAN Serine/threonine-protein kinase 4 (EC 2.7.1...	88 6e-17
<input type="checkbox"/>	sp	Q94804	STK10_HUMAN Serine/threonine-protein kinase 10 (EC 2.7...	88 6e-17
<input type="checkbox"/>	sp	P53671	LIMK2_HUMAN LIM domain kinase 2 (EC 2.7.11.1) (LIMK-2)...	88 6e-17
<input type="checkbox"/>	tr	Q9UFU0	_HUMAN Putative uncharacterized protein DKFZp586K0922 (...	88 6e-17
<input type="checkbox"/>	tr	A6ND35	_HUMAN Uncharacterized protein STK10 [STK10] [Homo sapi...	88 6e-17
<input type="checkbox"/>	tr	A0PJ51	_HUMAN STK4 protein (Fragment) [STK4] [Homo sapiens (Hu...	88 6e-17
<input type="checkbox"/>	sp_vs	P53671-2	Isoform LIMK2b of P53671 - Homo sapiens (Human) [...	88 6e-17
<input type="checkbox"/>	sp_vs	Q13043-2	Isoform 2 of Q13043 - Homo sapiens (Human) [STK4]...	88 6e-17
<input type="checkbox"/>	sp	Q16513	PKN2_HUMAN Serine/threonine-protein kinase N2 (EC 2.7....	87 8e-17
<input type="checkbox"/>	sp	Q96PY6	NEK1_HUMAN Serine/threonine-protein kinase Nek1 (EC 2....	87 8e-17
<input type="checkbox"/>	sp	Q96RW7	HMCN1_HUMAN Hemicentin-1 precursor (Fibulin-6) (FIBL-6...	87 8e-17
<input type="checkbox"/>	tr	Q86XJ6	_HUMAN Protein kinase C, delta (Protein kinase C, delta...	87 8e-17
<input type="checkbox"/>	tr	Q14CB7	_HUMAN NEK1 protein [NEK1] [Homo sapiens (Human)]	87 8e-17
<input type="checkbox"/>	tr	Q05DG5	_HUMAN NEK1 protein (Fragment) [NEK1] [Homo sapiens (Hu...	87 8e-17
<input type="checkbox"/>	tr	A6NGE3	_HUMAN Uncharacterized protein HMCN1 [HMCN1] [Homo sapi...	87 8e-17
<input type="checkbox"/>	sp_vs	Q96RW7-2	Isoform 2 of Q96RW7 - Homo sapiens (Human) [HMCN1...	87 8e-17
<input type="checkbox"/>	sp_vs	Q96PY6-2	Isoform 2 of Q96PY6 - Homo sapiens (Human) [NEK1]...	87 8e-17
<input type="checkbox"/>	sp_vs	Q13153-2	Isoform 2 of Q13153 - Homo sapiens (Human) [PAK1]...	87 8e-17
<input type="checkbox"/>	sp	Q05655	KPCD_HUMAN Protein kinase C delta type (EC 2.7.11.13) ...	87 1e-16
<input type="checkbox"/>	sp	Q00526	CDK3_HUMAN Cell division protein kinase 3 (EC 2.7.11.2...	87 1e-16
<input type="checkbox"/>	tr	Q5JPB0	_HUMAN Putative uncharacterized protein DKFZp434B079 [D...	87 1e-16
<input type="checkbox"/>	tr	Q5H9T1	_HUMAN Putative uncharacterized protein DKFZp686D06121 ...	87 1e-16
<input type="checkbox"/>	sp	Q96L34	MARK4_HUMAN MAP/microtubule affinity-regulating kinase...	87 1e-16
<input type="checkbox"/>	sp	Q9UQB9	AURKC_HUMAN Serine/threonine-protein kinase 13 (EC 2.7...	87 1e-16
<input type="checkbox"/>	sp_vs	Q96L34-2	Isoform 2 of Q96L34 - Homo sapiens (Human) [MARK4...	87 1e-16
<input type="checkbox"/>	sp	P17252	KPCA_HUMAN Protein kinase C alpha type (EC 2.7.11.13) ...	86 2e-16
<input type="checkbox"/>	tr	Q2TSD3	_HUMAN Aging-associated gene 6 protein [Homo sapiens (H...	86 2e-16
<input type="checkbox"/>	tr	Q5TSB4	_HUMAN Serine/threonine kinase 24 (STE20 homolog, yeast...	86 2e-16
<input type="checkbox"/>	sp	Q14965	STK6_HUMAN Serine/threonine-protein kinase 6 (EC 2.7.1...	86 3e-16
<input type="checkbox"/>	sp	Q13188	STK3_HUMAN Serine/threonine-protein kinase 3 (EC 2.7.1...	85 4e-16
<input type="checkbox"/>	sp	Q95747	OXSRL_HUMAN Serine/threonine-protein kinase OSR1 (EC 2...	85 4e-16
<input type="checkbox"/>	sp	Q60285	NUAK1_HUMAN NUA family SNF1-like kinase 1 (EC 2.7.11....	85 4e-16
<input type="checkbox"/>	tr	Q62NR9	_HUMAN CDNA FLJ27266 fis, clone TMS00356, highly simila...	85 4e-16
<input type="checkbox"/>	tr	A7MD39	_HUMAN NUA family, SNF1-like kinase, 1 (NUAK family, S...	85 4e-16
<input type="checkbox"/>	sp	Q00506	STK25_HUMAN Serine/threonine-protein kinase 25 (EC 2.7...	84 6e-16
<input type="checkbox"/>	sp	Q9HC98	NEK6_HUMAN Serine/threonine-protein kinase Nek6 (EC 2....	84 6e-16
<input type="checkbox"/>	sp	P06493	CDC2_HUMAN Cell division control protein 2 homolog (EC...	84 6e-16
<input type="checkbox"/>	tr	Q96BA2	_HUMAN STK25 protein [Homo sapiens (Human)]	84 6e-16
<input type="checkbox"/>	tr	Q6FG86	_HUMAN NEK6 protein (Fragment) [NEK6] [Homo sapiens (Hu...	84 6e-16
<input type="checkbox"/>	tr	Q5VZ16	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84 6e-16
<input type="checkbox"/>	tr	Q5VZ09	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	84 6e-16
<input type="checkbox"/>	sp	Q59H18	TNI3K_HUMAN Serine/threonine-protein kinase TNNI3K (EC...	84 8e-16

<input type="checkbox"/>	tr	Q6DLZ0	_HUMAN Aurora/Ipl1-related kinase 3 transcript variant ...	84	8e-16
<input type="checkbox"/>	tr	Q6AZY8	_HUMAN AURKC protein (Aurora kinase C, isoform CRA_a) [...	84	8e-16
<input type="checkbox"/>	tr	Q5Y191	_HUMAN Aurora-C [AURKC] [Homo sapiens (Human)]	84	8e-16
<input type="checkbox"/>	tr	Q3B785	_HUMAN CDC2 protein [CDC2] [Homo sapiens (Human)]	84	8e-16
<input type="checkbox"/>	tr	Q17RNO	_HUMAN TNNI3 interacting kinase [TNNI3K] [Homo sapiens ...	84	8e-16
<input type="checkbox"/>	sp_vs	Q9UQB9-2	Isoform 2 of Q9UQB9 - Homo sapiens (Human) [AURKC...	84	8e-16
<input type="checkbox"/>	sp_vs	Q59H18-2	Isoform 2 of Q59H18 - Homo sapiens (Human) [TNNI3...	84	8e-16
<input type="checkbox"/>	sp	Q94779	CNTN5_HUMAN Contactin-5 precursor (Neural recognition ...	84	1e-15
<input type="checkbox"/>	tr	Q49AF3	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
<input type="checkbox"/>	tr	A1L4P0	_HUMAN CNTN5 protein [CNTN5] [Homo sapiens (Human)]	84	1e-15
<input type="checkbox"/>	sp_vs	Q94779-2	Isoform 2 of Q94779 - Homo sapiens (Human) [CNTN5...	84	1e-15
<input type="checkbox"/>	sp_vs	Q9BYT3-2	Isoform 2 of Q9BYT3 - Homo sapiens (Human) [STK33...	84	1e-15
<input type="checkbox"/>	sp	Q56UN5	YSK4_HUMAN SPS1/STE20-related protein kinase YSK4 (EC ...	83	1e-15
<input type="checkbox"/>	sp	Q14680	MELK_HUMAN Maternal embryonic leucine zipper kinase (E...	83	1e-15
<input type="checkbox"/>	tr	Q5T263	_HUMAN Maternal embryonic leucine zipper kinase (Matern...	83	1e-15
<input type="checkbox"/>	tr	Q53GX0	_HUMAN Maternal embryonic leucine zipper kinase variant...	83	1e-15
<input type="checkbox"/>	sp_vs	Q56UN5-3	Isoform 3 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
<input type="checkbox"/>	sp_vs	Q56UN5-5	Isoform 5 of Q56UN5 - Homo sapiens (Human) [YSK4]...	83	1e-15
<input type="checkbox"/>	sp	Q00534	CDK6_HUMAN Cell division protein kinase 6 (EC 2.7.11.2...	83	2e-15
<input type="checkbox"/>	tr	Q5H9N4	_HUMAN Putative uncharacterized protein DKFZp686L20222 ...	83	2e-15
<input type="checkbox"/>	tr	A4D1G0	_HUMAN Cyclin-dependent kinase 6 (HCG19542) [CDK6] [Hom...	83	2e-15
<input type="checkbox"/>	sp	Q96GD4	AURKB_HUMAN Serine/threonine-protein kinase 12 (EC 2.7...	82	2e-15
<input type="checkbox"/>	tr	Q6IAR3	_HUMAN NEK6 protein [NEK6] [Homo sapiens (Human)]	82	2e-15
<input type="checkbox"/>	tr	A3KFX0	_HUMAN Aurora kinase A [AURKA] [Homo sapiens (Human)]	82	2e-15
<input type="checkbox"/>	tr	A2ABM8	_HUMAN Discoidin domain receptor family, member 1 (Frag...	82	2e-15
<input type="checkbox"/>	tr	A2ABL3	_HUMAN Discoidin domain receptor family, member 1 (Frag...	82	2e-15
<input type="checkbox"/>	sp	Q6P5Z2	PKN3_HUMAN Serine/threonine-protein kinase N3 (EC 2.7....	82	3e-15
<input type="checkbox"/>	tr	Q86VS1	_HUMAN Protein kinase, AMP-activated, alpha 1 catalytic...	82	3e-15
<input type="checkbox"/>	tr	Q7L3H5	_HUMAN LIM domain kinase 2 (LIM domain kinase 2, isofo...	82	3e-15
<input type="checkbox"/>	sp	P57059	SN1L1_HUMAN Serine/threonine-protein kinase SNF1-like ...	82	4e-15
<input type="checkbox"/>	sp	Q6ZN16	M3K15_HUMAN Mitogen-activated protein kinase kinase ki...	82	4e-15
<input type="checkbox"/>	sp	Q13131	AAPK1_HUMAN 5'-AMP-activated protein kinase catalytic ...	82	4e-15
<input type="checkbox"/>	sp_vs	Q6ZN16-2	Isoform 2 of Q6ZN16 - Homo sapiens (Human) [MAP3K...	82	4e-15
<input type="checkbox"/>	sp_vs	Q6ZN16-3	Isoform 3 of Q6ZN16 - Homo sapiens (Human) [MAP3K...	82	4e-15
<input type="checkbox"/>	sp	Q16512	PKN1_HUMAN Serine/threonine-protein kinase N1 (EC 2.7....	81	5e-15
<input type="checkbox"/>	sp	Q13177	PAK2_HUMAN Serine/threonine-protein kinase PAK 2 (EC 2...	81	5e-15
<input type="checkbox"/>	sp_vs	Q9UPZ9-2	Isoform 2 of Q9UPZ9 - Homo sapiens (Human) [ICK] ...	81	5e-15
<input type="checkbox"/>	sp	Q9H4B4	PLK3_HUMAN Serine/threonine-protein kinase PLK3 (EC 2....	81	7e-15
<input type="checkbox"/>	sp	Q8NG66	NEK11_HUMAN Serine/threonine-protein kinase Nek11 (EC ...	81	7e-15
<input type="checkbox"/>	sp	Q9UK32	KS6A6_HUMAN Ribosomal protein S6 kinase alpha-6 (EC 2....	81	7e-15
<input type="checkbox"/>	sp	Q9NWZ3	IRAK4_HUMAN Interleukin-1 receptor-associated kinase 4...	81	7e-15
<input type="checkbox"/>	sp	Q9UPZ9	ICK_HUMAN Serine/threonine-protein kinase ICK (EC 2.7....	81	7e-15
<input type="checkbox"/>	sp	Q9P232	CNTN3_HUMAN Contactin-3 precursor (Brain-derived immun...	81	7e-15
<input type="checkbox"/>	tr	Q69FE3	_HUMAN Interleukin-1 receptor-associated kinase 4 varia...	81	7e-15
<input type="checkbox"/>	tr	Q5JR99	_HUMAN Polo-like kinase 3 (Drosophila) [PLK3] [Homo sap...	81	7e-15
<input type="checkbox"/>	tr	Q75271	_HUMAN R31237_1, (Fragment) [Homo sapiens (Human)]	81	7e-15
<input type="checkbox"/>	tr	A7MD41	_HUMAN Intestinal cell (MAK-like) kinase (Intestinal ce...	81	7e-15
<input type="checkbox"/>	tr	A6NKA6	_HUMAN Uncharacterized protein CDKL5 [CDKL5] [Homo sapi...	81	7e-15
<input type="checkbox"/>	tr	A6NHD7	_HUMAN Uncharacterized protein NEK11 [NEK11] [Homo sapi...	81	7e-15
<input type="checkbox"/>	sp_vs	Q8NG66-2	Isoform 2 of Q8NG66 - Homo sapiens (Human) [NEK11...	81	7e-15
<input type="checkbox"/>	sp_vs	Q8NG66-3	Isoform 3 of Q8NG66 - Homo sapiens (Human) [NEK11...	81	7e-15
<input type="checkbox"/>	sp	Q13153	PAK1_HUMAN Serine/threonine-protein kinase PAK 1 (EC 2...	80	9e-15
<input type="checkbox"/>	sp	Q99683	M3K5_HUMAN Mitogen-activated protein kinase kinase kin...	80	9e-15
<input type="checkbox"/>	tr	Q6ZNI2	_HUMAN CDNA FLJ16039 fis, clone ADRGL2001554, weakly si...	80	9e-15
<input type="checkbox"/>	tr	Q59GL6	_HUMAN Mitogen-activated protein kinase kinase kinase 5...	80	9e-15
<input type="checkbox"/>	tr	A6NKM9	_HUMAN Uncharacterized protein MAP3K5 (Fragment) [MAP3K...	80	9e-15
<input type="checkbox"/>	tr	A6NIA0	_HUMAN Uncharacterized protein MAP3K5 [MAP3K5] [Homo sa...	80	9e-15
<input type="checkbox"/>	sp	Q9BYT3	STK33_HUMAN Serine/threonine-protein kinase 33 (EC 2.7...	80	1e-14
<input type="checkbox"/>	sp	Q9NYY3	PLK2_HUMAN Serine/threonine-protein kinase PLK2 (EC 2....	80	1e-14
<input type="checkbox"/>	sp	Q8IVH8	M4K3_HUMAN Mitogen-activated protein kinase kinase kin...	80	1e-14
<input type="checkbox"/>	sp	P54646	AAPK2_HUMAN 5'-AMP-activated protein kinase catalytic ...	80	1e-14
<input type="checkbox"/>	tr	Q92626	_HUMAN Peroxidase homolog (Melanoma-associated antigen...	80	1e-14
<input type="checkbox"/>	tr	Q8N7M6	_HUMAN CDNA FLJ40844 fis, clone TRACH2014356, highly si...	80	1e-14
<input type="checkbox"/>	tr	Q6IQ39	_HUMAN MAP4K3 protein (Mitogen-activated protein kinase...	80	1e-14
<input type="checkbox"/>	tr	Q69FE1	_HUMAN Interleukin-1 receptor-associated kinase 4 short...	80	1e-14
<input type="checkbox"/>	tr	Q4KXG2	_HUMAN PXDN protein (Fragment) [PXDN] [Homo sapiens (Hu...	80	1e-14

<input type="checkbox"/>	sp_vs	Q8IVH8-3	Isoform 3 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	80	1e-14
<input type="checkbox"/>	sp	Q9UKE5	TNIK_HUMAN TRAF2 and NCK-interacting protein kinase (E...	80	2e-14
<input type="checkbox"/>	sp	P20794	MAK_HUMAN Serine/threonine-protein kinase MAK (EC 2.7....	80	2e-14
<input type="checkbox"/>	sp	P57058	HUNK_HUMAN Hormonally up-regulated neu tumor-associate...	80	2e-14
<input type="checkbox"/>	sp	O76039	CDKL5_HUMAN Cyclin-dependent kinase-like 5 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	sp	Q92772	CDKL2_HUMAN Cyclin-dependent kinase-like 2 (EC 2.7.11....	80	2e-14
<input type="checkbox"/>	tr	Q8IXN4	_HUMAN MAK protein [Homo sapiens (Human)]	80	2e-14
<input type="checkbox"/>	tr	Q547D0	_HUMAN Male germ cell-associated kinase (Male germ cell...	80	2e-14
<input type="checkbox"/>	tr	A7E2A3	_HUMAN TRAF2 and NCK interacting kinase (TRAF2 and NCK ...	80	2e-14
<input type="checkbox"/>	tr	A0MZP5	_HUMAN AMP-activated alpha 2 subunit [PRKAA2] [Homo sap...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-2	Isoform 2 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-3	Isoform 3 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-4	Isoform 4 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-5	Isoform 5 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-6	Isoform 6 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-7	Isoform 7 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp_vs	Q9UKE5-8	Isoform 8 of Q9UKE5 - Homo sapiens (Human) [TNIK]...	80	2e-14
<input type="checkbox"/>	sp	Q00537	PCTK2_HUMAN Serine/threonine-protein kinase PCTAIRE-2 ...	79	2e-14
<input type="checkbox"/>	sp	Q8TD19	NEK9_HUMAN Serine/threonine-protein kinase Nek9 (EC 2....	79	2e-14
<input type="checkbox"/>	sp	Q8IYW2	CNTN4_HUMAN Contactin-4 precursor (Brain-derived immun...	79	2e-14
<input type="checkbox"/>	tr	Q59FN2	_HUMAN P21-activated kinase 2 variant (Fragment) [Homo ...	79	2e-14
<input type="checkbox"/>	sp_vs	Q8IYW2-3	Isoform 3 of Q8IYW2 - Homo sapiens (Human) [CNTN4...	79	2e-14
<input type="checkbox"/>	sp	Q8IYT8	ULK2_HUMAN Serine/threonine-protein kinase ULK2 (EC 2....	79	3e-14
<input type="checkbox"/>	sp	Q8IVT5	KSR1_HUMAN Kinase suppressor of Ras 1 [KSR1] [Homo sap...	79	3e-14
<input type="checkbox"/>	sp	Q4KMG0	CDON_HUMAN Cell adhesion molecule-related/down-regulat...	79	3e-14
<input type="checkbox"/>	tr	Q8NC04	_HUMAN CDNA FLJ90626 fis, clone PLACE1003135, weakly si...	79	3e-14
<input type="checkbox"/>	tr	Q15523	_HUMAN Serine/threonine protein kinase [Homo sapiens (H...	79	3e-14
<input type="checkbox"/>	sp_vs	Q4KMG0-2	Isoform 2 of Q4KMG0 - Homo sapiens (Human) [CDON]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-2	Isoform 2 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp_vs	Q8IVT5-3	Isoform 3 of Q8IVT5 - Homo sapiens (Human) [KSR1]...	79	3e-14
<input type="checkbox"/>	sp	Q15759	MK11_HUMAN Mitogen-activated protein kinase 11 (EC 2.7...	79	4e-14
<input type="checkbox"/>	sp	P51841	GUC2F_HUMAN Retinal guanylyl cyclase 2 precursor (EC 4...	79	4e-14
<input type="checkbox"/>	tr	Q86VU3	_HUMAN MAP4K2 protein (Mitogen-activated protein kinase...	79	4e-14
<input type="checkbox"/>	sp_vs	Q96S53-2	Isoform 2 of Q96S53 - Homo sapiens (Human) [TESK2...	79	4e-14
<input type="checkbox"/>	sp	Q8N4C8	MINK1_HUMAN Misshapen-like kinase 1 (EC 2.7.11.1) (Mit...	78	5e-14
<input type="checkbox"/>	sp	Q92918	M4K1_HUMAN Mitogen-activated protein kinase kinase kin...	78	5e-14
<input type="checkbox"/>	sp	Q8IVW4	CDKL3_HUMAN Cyclin-dependent kinase-like 3 (EC 2.7.11....	78	5e-14
<input type="checkbox"/>	tr	Q5U8Z0	_HUMAN Misshapen/NIKs-related kinase isoform beta [MINK...	78	5e-14
<input type="checkbox"/>	tr	Q5JPK7	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IVW4-2	Isoform 2 of Q8IVW4 - Homo sapiens (Human) [CDKL3...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8IVH8-2	Isoform 2 of Q8IVH8 - Homo sapiens (Human) [MAP4K...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-2	Isoform 1 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q8N4C8-3	Isoform 2 of Q8N4C8 - Homo sapiens (Human) [MINK1...	78	5e-14
<input type="checkbox"/>	sp_vs	Q59H18-4	Isoform 4 of Q59H18 - Homo sapiens (Human) [TNIN3...	78	5e-14
<input type="checkbox"/>	sp	O75914	PAK3_HUMAN Serine/threonine-protein kinase PAK 3 (EC 2...	78	6e-14
<input type="checkbox"/>	sp	O95819	M4K4_HUMAN Mitogen-activated protein kinase kinase kin...	78	6e-14
<input type="checkbox"/>	tr	Q6ZMM4	_HUMAN CDNA FLJ16821 fis, clone TRACH3021066, highly si...	78	6e-14
<input type="checkbox"/>	tr	Q59ED6	_HUMAN Polo-like kinase 3 variant (Fragment) [Homo sapi...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-2	Isoform 2 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-3	Isoform 3 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-4	Isoform 4 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O95819-5	Isoform 5 of O95819 - Homo sapiens (Human) [MAP4K...	78	6e-14
<input type="checkbox"/>	sp_vs	O75914-2	Isoform 2 of O75914 - Homo sapiens (Human) [PAK3]...	78	6e-14
<input type="checkbox"/>	sp	O75385	ULK1_HUMAN Serine/threonine-protein kinase ULK1 (EC 2....	77	8e-14
<input type="checkbox"/>	sp	Q96PF2	TSSK2_HUMAN Testis-specific serine/threonine-protein k...	77	8e-14
<input type="checkbox"/>	sp	Q7L7X3	TAOK1_HUMAN Serine/threonine-protein kinase TAO1 (EC 2...	77	8e-14
<input type="checkbox"/>	sp	Q12851	M4K2_HUMAN Mitogen-activated protein kinase kinase kin...	77	8e-14
<input type="checkbox"/>	sp	P05129	KPCG_HUMAN Protein kinase C gamma type (EC 2.7.11.13) ...	77	8e-14
<input type="checkbox"/>	tr	Q6A1A2	_HUMAN PDPK2 protein [PDPK2] [Homo sapiens (Human)]	77	8e-14
<input type="checkbox"/>	tr	A2RUT8	_HUMAN TAO kinase 1 (TAO kinase 1, isoform CRA_a) [TAOK...	77	8e-14
<input type="checkbox"/>	tr	A0ZT99	_HUMAN Testis-specific serine kinase 2 (HCG1641087) [TS...	77	8e-14
<input type="checkbox"/>	sp	P53350	PLK1_HUMAN Serine/threonine-protein kinase PLK1 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	Q14012	KCC1A_HUMAN Calcium/calmodulin-dependent protein kinas...	77	1e-13
<input type="checkbox"/>	sp_vs	Q96RW7-3	Isoform 3 of Q96RW7 - Homo sapiens (Human) [HMCN1...	77	1e-13
<input type="checkbox"/>	sp	Q6PHR2	ULK3_HUMAN Serine/threonine-protein kinase ULK3 (EC 2....	77	1e-13
<input type="checkbox"/>	sp	O15530	PDPK1_HUMAN 3-phosphoinositide-dependent protein kinas...	77	1e-13

<input type="checkbox"/>	sp	Q00536	PCTK1_HUMAN Serine/threonine-protein kinase PCTAIRE-1 ...	77	1e-13
<input type="checkbox"/>	sp	Q16539	MK14_HUMAN Mitogen-activated protein kinase 14 (EC 2.7...	77	1e-13
<input type="checkbox"/>	tr	Q9UPJ8	_HUMAN PkB-like (Fragment) [PkB-like 1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q9BRL4	_HUMAN PCTK1 protein [PCTK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q96GA5	_HUMAN PCTK1 protein (Fragment) [PCTK1] [Homo sapiens (...]	77	1e-13
<input type="checkbox"/>	tr	Q6FI20	_HUMAN PDPK1 protein [PDPK1] [Homo sapiens (Human)]	77	1e-13
<input type="checkbox"/>	tr	Q59EH6	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	77	1e-13
<input type="checkbox"/>	tr	A6P3A7	_HUMAN Maternal embryonic leucine zipper kinase v2 [MEL...	77	1e-13
<input type="checkbox"/>	sp_vs	P11362-15	Isoform 16 of P11362 - Homo sapiens (Human) [FGF...	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-3	Isoform Mxi2 of Q16539 - Homo sapiens (Human) [MA...	77	1e-13
<input type="checkbox"/>	sp_vs	Q16539-4	Isoform Ezip of Q16539 - Homo sapiens (Human) [MA...	77	1e-13
<input type="checkbox"/>	sp_vs	Q15530-2	Isoform 2 of Q15530 - Homo sapiens (Human) [PDPK1...	77	1e-13
<input type="checkbox"/>	sp	Q9HCK4	ROBO2_HUMAN Roundabout homolog 2 precursor [ROBO2] [Ho...	76	2e-13
<input type="checkbox"/>	sp	Q9UQ07	MOK_HUMAN MAPK/MAK/MRK overlapping kinase (EC 2.7.11.2...	76	2e-13
<input type="checkbox"/>	sp	Q55007	LRRK2_HUMAN Leucine-rich repeat serine/threonine-prote...	76	2e-13
<input type="checkbox"/>	tr	Q19AB5	_HUMAN ROBO2 isoform a [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	tr	Q19AB4	_HUMAN ROBO2 isoform b (Roundabout, axon guidance recep...	76	2e-13
<input type="checkbox"/>	tr	Q17RV3	_HUMAN Leucine-rich repeat kinase 2 [LRRK2] [Homo sapie...	76	2e-13
<input type="checkbox"/>	tr	A6NJU2	_HUMAN Uncharacterized protein LRRK2 [LRRK2] [Homo sapi...	76	2e-13
<input type="checkbox"/>	tr	A6NC84	_HUMAN Uncharacterized protein SNF1LK [SNF1LK] [Homo sa...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9UQ07-2	Isoform 2 of Q9UQ07 - Homo sapiens (Human) [RAGE]...	76	2e-13
<input type="checkbox"/>	sp_vs	Q9HCK4-2	Isoform 2 of Q9HCK4 - Homo sapiens (Human) [ROBO2...	76	2e-13
<input type="checkbox"/>	sp	Q8WZ42	TITIN_HUMAN Titin (EC 2.7.11.1) (Connectin) (Rhabdomyo...	76	2e-13
<input type="checkbox"/>	sp	Q9Y2K2	QSK_HUMAN Serine/threonine-protein kinase QSK (EC 2.7...	76	2e-13
<input type="checkbox"/>	sp	Q00535	CDK5_HUMAN Cell division protein kinase 5 (EC 2.7.11.2...	76	2e-13
<input type="checkbox"/>	tr	Q9NWX4	_HUMAN CDNA FLJ20549 fis, clone KAT11561 [Homo sapiens ...]	76	2e-13
<input type="checkbox"/>	tr	A6NI10	_HUMAN Uncharacterized protein ENSP00000364441 [Homo sa...	76	2e-13
<input type="checkbox"/>	tr	A1A5A8	_HUMAN KIAA0999 protein [KIAA0999] [Homo sapiens (Human)]	76	2e-13
<input type="checkbox"/>	sp_vs	Q9Y2K2-3	Isoform 3 of Q9Y2K2 - Homo sapiens (Human) [QSK] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-2	Isoform 2 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-4	Isoform 4 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-5	Isoform 5 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-7	Isoform 7 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp_vs	Q8WZ42-8	Isoform 8 of Q8WZ42 - Homo sapiens (Human) [TTN] ...	76	2e-13
<input type="checkbox"/>	sp	Q9NQU5	PAK6_HUMAN Serine/threonine-protein kinase PAK 6 (EC 2...	75	3e-13
<input type="checkbox"/>	sp	Q7Z2Y5	NRK_HUMAN Nik-related protein kinase (EC 2.7.11.1) [NR...	75	3e-13
<input type="checkbox"/>	sp	Q6VAB6	KSR2_HUMAN Kinase suppressor of Ras 2 (hKSR2) [KSR2] [...]	75	3e-13
<input type="checkbox"/>	sp	P24941	CDK2_HUMAN Cell division protein kinase 2 (EC 2.7.11.2...	75	3e-13
<input type="checkbox"/>	tr	Q59GT1	_HUMAN Conserved helix-loop-helix ubiquitous kinase var...	75	3e-13
<input type="checkbox"/>	tr	Q53HJ9	_HUMAN 3-phosphoinositide dependent protein kinase-1 va...	75	3e-13
<input type="checkbox"/>	tr	A7E2B2	_HUMAN CRKRS protein [CRKRS] [Homo sapiens (Human)]	75	3e-13
<input type="checkbox"/>	sp	Q9P286	PAK7_HUMAN Serine/threonine-protein kinase PAK 7 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	Q8IY84	NIM1_HUMAN Serine/threonine-protein kinase NIM1 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	P51955	NEK2_HUMAN Serine/threonine-protein kinase Nek2 (EC 2...	75	4e-13
<input type="checkbox"/>	sp	O15111	IKKA_HUMAN Inhibitor of nuclear factor kappa-B kinase ...	75	4e-13
<input type="checkbox"/>	sp	P11802	CDK4_HUMAN Cell division protein kinase 4 (EC 2.7.11.2...	75	4e-13
<input type="checkbox"/>	sp	Q9NYV4	CD2L7_HUMAN Cell division cycle 2-related protein kina...	75	4e-13
<input type="checkbox"/>	sp	Q14004	CD2L5_HUMAN Cell division cycle 2-like protein kinase ...	75	4e-13
<input type="checkbox"/>	tr	Q9BVE2	_HUMAN CDC2L5 protein [Homo sapiens (Human)]	75	4e-13
<input type="checkbox"/>	tr	Q8TB93	_HUMAN P21(CDKN1A)-activated kinase 7 [PAK7] [Homo sapi...	75	4e-13
<input type="checkbox"/>	tr	Q6PG61	_HUMAN CDK4 protein (Cyclin-dependent kinase 4, isoform...	75	4e-13
<input type="checkbox"/>	tr	Q562E6	_HUMAN Conserved helix-loop-helix ubiquitous kinase [CH...	75	4e-13
<input type="checkbox"/>	sp_vs	Q14004-2	Isoform 2 of Q14004 - Homo sapiens (Human) [CDC2L...	75	4e-13
<input type="checkbox"/>	sp_vs	Q16539-2	Isoform CSBP1 of Q16539 - Homo sapiens (Human) [M...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-2	Isoform 2 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp_vs	P51955-3	Isoform 3 of P51955 - Homo sapiens (Human) [NEK2]...	75	4e-13
<input type="checkbox"/>	sp	Q9H2K8	TAO3_HUMAN Serine/threonine-protein kinase TAO3 (EC 2...	75	5e-13
<input type="checkbox"/>	sp	Q9UZE5	ST17A_HUMAN Serine/threonine-protein kinase 17A (EC 2...	75	5e-13
<input type="checkbox"/>	sp	Q07002	PCTK3_HUMAN Serine/threonine-protein kinase PCTAIRE-3 ...	75	5e-13
<input type="checkbox"/>	sp	Q9NZJ5	E2AK3_HUMAN Eukaryotic translation initiation factor 2...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A3	_HUMAN PCTAIRE protein kinase 3 isoform a (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6V3A2	_HUMAN PCTAIRE protein kinase 3 isoform b (PCTAIRE prot...	75	5e-13
<input type="checkbox"/>	tr	Q6IAW3	_HUMAN CDK5 protein [CDK5] [Homo sapiens (Human)]	75	5e-13
<input type="checkbox"/>	tr	Q68DI6	_HUMAN Putative uncharacterized protein DKFZp781H1925 [...]	75	5e-13
<input type="checkbox"/>	tr	Q59G02	_HUMAN PCTAIRE protein kinase 3 isoform b variant (Frag...	75	5e-13
<input type="checkbox"/>	tr	Q53QY0	_HUMAN Putative uncharacterized protein EIF2AK3 (Fragme...	75	5e-13

<input type="checkbox"/>	tr	A4D1V6	_HUMAN Serine/threonine kinase 17a (Apoptosis-inducing)...	75	5e-13
<input type="checkbox"/>	tr	AOAVI1	_HUMAN Eukaryotic translation initiation factor 2-alpha...	75	5e-13
<input type="checkbox"/>	sp	Q8NEV4	MYO3A_HUMAN Myosin IIIA (EC 2.7.11.1) [MYO3A] [Homo sa...	74	7e-13
<input type="checkbox"/>	sp	Q9UQ52	CNTN6_HUMAN Contactin-6 precursor (Neural recognition ...	74	7e-13
<input type="checkbox"/>	tr	Q9Y6B5	_HUMAN PAK2 [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q6ZWT8	_HUMAN CDNA FLJ14395 fis, clone HEMBA1003250, weakly si...	74	7e-13
<input type="checkbox"/>	tr	Q5VXI3	_HUMAN Myosin IIIA [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q0VD65	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	tr	Q05AG9	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	74	7e-13
<input type="checkbox"/>	sp	Q15831	STK11_HUMAN Serine/threonine-protein kinase 11 (EC 2.7...	74	9e-13
<input type="checkbox"/>	sp	O00444	PLK4_HUMAN Serine/threonine-protein kinase PLK4 (EC 2...	74	9e-13
<input type="checkbox"/>	sp	P23443	KS6B1_HUMAN Ribosomal protein S6 kinase beta-1 (EC 2.7...	74	9e-13
<input type="checkbox"/>	tr	Q9HBS3	_HUMAN Putative uncharacterized protein [Homo sapiens (...	74	9e-13
<input type="checkbox"/>	tr	Q7Z721	_HUMAN RPS6KB1 protein (Ribosomal protein S6 kinase, 70...	74	9e-13
<input type="checkbox"/>	sp_vs	P23443-2	Isoform Alpha II of P23443 - Homo sapiens (Human)...	74	9e-13
<input type="checkbox"/>	sp	O94856	NFASC_HUMAN Neurofascin precursor [NFASC] [Homo sapien...	74	1e-12
<input type="checkbox"/>	tr	Q9H4D1	_HUMAN Protein kinase [dik] [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	tr	Q2TB16	_HUMAN Receptor-interacting serine-threonine kinase 4 (...	74	1e-12
<input type="checkbox"/>	tr	Q15879	_HUMAN Protein kinase (Fragment) [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	tr	Q149P5	_HUMAN NFASC protein [NFASC] [Homo sapiens (Human)]	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-2	Isoform 2 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-3	Isoform 3 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-4	Isoform 4 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-5	Isoform 5 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-6	Isoform 6 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-7	Isoform 7 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-8	Isoform 8 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-9	Isoform 9 of O94856 - Homo sapiens (Human) [NFASC...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-10	Isoform 10 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-11	Isoform 11 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-12	Isoform 12 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	O94856-13	Isoform 13 of O94856 - Homo sapiens (Human) [NFA...	74	1e-12
<input type="checkbox"/>	sp_vs	P57078-2	Isoform 2 of P57078 - Homo sapiens (Human) [RIPK4...	74	1e-12
<input type="checkbox"/>	sp	O95382	M3K6_HUMAN Mitogen-activated protein kinase kinase kin...	73	1e-12
<input type="checkbox"/>	tr	Q5TI62	_HUMAN Ribosomal protein S6 kinase, 90kDa, polypeptide ...	73	1e-12
<input type="checkbox"/>	tr	Q5SSD4	_HUMAN Mitogen-activated protein kinase kinase kinase 6...	73	1e-12
<input type="checkbox"/>	tr	Q32MQ5	_HUMAN MAP3K6 protein [MAP3K6] [Homo sapiens (Human)]	73	1e-12
<input type="checkbox"/>	sp_vs	O95382-2	Isoform 2 of O95382 - Homo sapiens (Human) [MAP3K...	73	1e-12
<input type="checkbox"/>	sp_vs	O95382-3	Isoform 3 of O95382 - Homo sapiens (Human) [MAP3K...	73	1e-12
<input type="checkbox"/>	sp_vs	Q56UN5-4	Isoform 4 of Q56UN5 - Homo sapiens (Human) [YSK4]...	73	1e-12
<input type="checkbox"/>	sp	Q9BXA6	TSSK6_HUMAN Testis-specific serine/threonine-protein k...	73	2e-12
<input type="checkbox"/>	sp	Q5MAI5	CDKL4_HUMAN Cyclin-dependent kinase-like 4 (EC 2.7.11...	73	2e-12
<input type="checkbox"/>	tr	Q8NDA2	_HUMAN Hemicentin-2 (Fragment) [DKFZp434P0216] [Homo sa...	73	2e-12
<input type="checkbox"/>	tr	Q2NME9	_HUMAN Cyclin-dependent kinase-like 4 [CDKL4] [Homo sap...	73	2e-12
<input type="checkbox"/>	sp	Q9Y4K4	M4K5_HUMAN Mitogen-activated protein kinase kinase kin...	72	3e-12
<input type="checkbox"/>	tr	Q5VZ10	_HUMAN NIMA (Never in mitosis gene a)-related kinase 6 ...	72	3e-12
<input type="checkbox"/>	tr	Q53GK9	_HUMAN MAPK13 protein variant (Fragment) [Homo sapiens ...	72	3e-12
<input type="checkbox"/>	sp	Q15746	MYLK_HUMAN Myosin light chain kinase, smooth muscle (E...	72	3e-12
<input type="checkbox"/>	sp	P11801	KPSH1_HUMAN Serine/threonine-protein kinase H1 (EC 2.7...	72	3e-12
<input type="checkbox"/>	sp	Q9C098	DCLK3_HUMAN Serine/threonine-protein kinase DCLK3 (EC ...	72	3e-12
<input type="checkbox"/>	sp	Q00532	CDKL1_HUMAN Cyclin-dependent kinase-like 1 (EC 2.7.11...	72	3e-12
<input type="checkbox"/>	tr	Q2M3A4	_HUMAN Cyclin-dependent kinase-like 1 (CDC2-related kin...	72	3e-12
<input type="checkbox"/>	sp_vs	Q15746-2	Isoform 2 of Q15746 - Homo sapiens (Human) [MYLK]...	72	3e-12
<input type="checkbox"/>	sp_vs	Q15746-6	Isoform Del-1790 of Q15746 - Homo sapiens (Human)...	72	3e-12
<input type="checkbox"/>	sp	O15264	MK13_HUMAN Mitogen-activated protein kinase 13 (EC 2.7...	72	4e-12
<input type="checkbox"/>	sp	Q02156	KPCE_HUMAN Protein kinase C epsilon type (EC 2.7.11.13...	72	4e-12
<input type="checkbox"/>	sp	P50750	CDK9_HUMAN Cell division protein kinase 9 (EC 2.7.11.2...	72	4e-12
<input type="checkbox"/>	tr	Q96T11	_HUMAN CDNA FLJ14518 fis, clone NT2RM1000850, weakly si...	72	4e-12
<input type="checkbox"/>	tr	Q6FI46	_HUMAN MAPK13 protein (Mitogen-activated protein kinase...	72	4e-12
<input type="checkbox"/>	tr	Q6FHR4	_HUMAN MAPK13 protein (Fragment) [MAPK13] [Homo sapiens...	72	4e-12
<input type="checkbox"/>	tr	A6YR18	_HUMAN Polarization-related protein LKB1 [Homo sapiens ...	72	4e-12
<input type="checkbox"/>	sp_vs	P50750-2	Isoform 2 of P50750 - Homo sapiens (Human) [CDK9]...	72	4e-12
<input type="checkbox"/>	sp	Q92823	NRCAM_HUMAN Neuronal cell adhesion molecule precursor ...	71	6e-12
<input type="checkbox"/>	sp	Q8WXR4	MYO3B_HUMAN Myosin-IIIB (EC 2.7.11.1) [MYO3B] [Homo sa...	71	6e-12
<input type="checkbox"/>	sp	Q8NFD2	ANKK1_HUMAN Ankyrin repeat and protein kinase domain-c...	71	6e-12
<input type="checkbox"/>	tr	Q59FI5	_HUMAN Protein kinase C, alpha variant (Fragment) [Homo...	71	6e-12

<input type="checkbox"/>	tr	Q4KM07	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	Q14CA1	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	Q14BM2	_HUMAN NRCAM protein [NRCAM] [Homo sapiens (Human)]	71	6e-12
<input type="checkbox"/>	tr	A4D0S3	_HUMAN Neuronal cell adhesion molecule (Neuronal cell a...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-2	Isoform 2 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-3	Isoform 3 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-4	Isoform 4 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-5	Isoform 5 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-6	Isoform 6 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q8WXR4-7	Isoform 7 of Q8WXR4 - Homo sapiens (Human) [MYO3B...	71	6e-12
<input type="checkbox"/>	sp_vs	Q92823-2	Isoform 2 of Q92823 - Homo sapiens (Human) [NRCAM...	71	6e-12
<input type="checkbox"/>	sp_vs	Q92823-3	Isoform 3 of Q92823 - Homo sapiens (Human) [NRCAM...	71	6e-12
<input type="checkbox"/>	sp_vs	Q92823-4	Isoform 4 of Q92823 - Homo sapiens (Human) [NRCAM...	71	6e-12
<input type="checkbox"/>	sp_vs	Q92823-5	Isoform 5 of Q92823 - Homo sapiens (Human) [NRCAM...	71	6e-12
<input type="checkbox"/>	sp	Q9UL54	TAOK2_HUMAN Serine/threonine-protein kinase TAO2 (EC 2...	71	7e-12
<input type="checkbox"/>	sp	Q99759	M3K3_HUMAN Mitogen-activated protein kinase kinase kin...	71	7e-12
<input type="checkbox"/>	tr	Q96HN9	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	71	7e-12
<input type="checkbox"/>	tr	Q8N3I9	_HUMAN Putative uncharacterized protein DKFPz762P223 (M...	71	7e-12
<input type="checkbox"/>	tr	Q86V37	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (...]	71	7e-12
<input type="checkbox"/>	tr	Q6PIN8	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (...]	71	7e-12
<input type="checkbox"/>	tr	Q1PBM3	_HUMAN Mitogen-activated protein kinase kinase kinase 3...	71	7e-12
<input type="checkbox"/>	tr	A7MCZ2	_HUMAN TAO kinase 2 (TAO kinase 2, isoform CRA_b) [TAOK...	71	7e-12
<input type="checkbox"/>	tr	A0PJ48	_HUMAN TAOK2 protein (Fragment) [TAOK2] [Homo sapiens (...]	71	7e-12
<input type="checkbox"/>	sp_vs	Q9UL54-2	Isoform 2 of Q9UL54 - Homo sapiens (Human) [TAOK2...	71	7e-12
<input type="checkbox"/>	sp	Q6SA08	TSSK4_HUMAN Testis-specific serine/threonine-protein k...	70	1e-11
<input type="checkbox"/>	sp	Q7Z5N4	SDK1_HUMAN Protein sidekick-1 precursor [SDK1] [Homo s...	70	1e-11
<input type="checkbox"/>	sp	Q5VST9	OBSCN_HUMAN Obscurin (EC 2.7.11.1) (Obscurin-myosin li...	70	1e-11
<input type="checkbox"/>	tr	Q6LD09	_HUMAN Tyrosine kinase (Fragment) [Homo sapiens (Human)]	70	1e-11
<input type="checkbox"/>	tr	Q5VXI1	_HUMAN Myosin IIIA (MYO3A protein) [MYO3A] [Homo sapien...	70	1e-11
<input type="checkbox"/>	tr	A2A391	_HUMAN Obscurin, cytoskeletal calmodulin and titin-inte...	70	1e-11
<input type="checkbox"/>	sp_vs	Q5VST9-2	Isoform 2 of Q5VST9 - Homo sapiens (Human) [OBSCN...	70	1e-11
<input type="checkbox"/>	sp_vs	Q5VST9-3	Isoform 3 of Q5VST9 - Homo sapiens (Human) [OBSCN...	70	1e-11
<input type="checkbox"/>	sp_vs	Q5VST9-6	Isoform 6 of Q5VST9 - Homo sapiens (Human) [OBSCN...	70	1e-11
<input type="checkbox"/>	sp_vs	Q7Z5N4-3	Isoform 3 of Q7Z5N4 - Homo sapiens (Human) [SDK1]...	70	1e-11
<input type="checkbox"/>	sp	Q9BXA7	TSSK1_HUMAN Testis-specific serine/threonine-protein k...	70	1e-11
<input type="checkbox"/>	sp	Q9NRH2	SNRK_HUMAN SNF-related serine/threonine-protein kinase...	70	1e-11
<input type="checkbox"/>	sp	P57078	RIPK4_HUMAN Receptor-interacting serine/threonine-prot...	70	1e-11
<input type="checkbox"/>	sp	Q02246	CNTN2_HUMAN Contactin-2 precursor (Axonin-1) (Axonal g...	70	1e-11
<input type="checkbox"/>	tr	Q8NCE6	_HUMAN CDNA FLJ90299 fis, clone NT2RP2000514, highly si...	70	1e-11
<input type="checkbox"/>	tr	Q59FA7	_HUMAN Serine/threonine protein kinase 11 variant (Frag...	70	1e-11
<input type="checkbox"/>	tr	Q53TX8	_HUMAN Putative uncharacterized protein MAP4K4 (Fragmen...	70	1e-11
<input type="checkbox"/>	tr	A1L3A3	_HUMAN Contactin 2 (Axonal) [CNTN2] [Homo sapiens (Human)]	70	1e-11
<input type="checkbox"/>	tr	A0ZT98	_HUMAN Testis-specific serine kinase 1 [TSSK1] [Homo sa...	70	1e-11
<input type="checkbox"/>	sp	O96013	PAK4_HUMAN Serine/threonine-protein kinase PAK 4 (EC 2...	70	2e-11
<input type="checkbox"/>	sp	P13592	NCA12_HUMAN Neural cell adhesion molecule 1, 120 kDa i...	70	2e-11
<input type="checkbox"/>	sp	P13591	NCA11_HUMAN Neural cell adhesion molecule 1, 140 kDa i...	70	2e-11
<input type="checkbox"/>	sp	Q9NR99	MXRAS_HUMAN Matrix-remodeling-associated protein 5 pre...	70	2e-11
<input type="checkbox"/>	tr	Q59FL7	_HUMAN Neural cell adhesion molecule 1, 120 kDa isoform...	70	2e-11
<input type="checkbox"/>	sp_vs	P13592-1	Isoform C of P13592 - Homo sapiens (Human) [NCAM1...	70	2e-11
<input type="checkbox"/>	sp_vs	O96013-2	Isoform 2 of O96013 - Homo sapiens (Human) [PAK4]...	70	2e-11
<input type="checkbox"/>	sp_vs	O96013-3	Isoform 3 of O96013 - Homo sapiens (Human) [PAK4]...	70	2e-11
<input type="checkbox"/>	sp_vs	O96013-4	Isoform 4 of O96013 - Homo sapiens (Human) [PAK4]...	70	2e-11
<input type="checkbox"/>	sp_vs	Q9NRH2-2	Isoform 2 of Q9NRH2 - Homo sapiens (Human) [SNRK]...	70	2e-11
<input type="checkbox"/>	sp	Q96MS0	ROBO3_HUMAN Roundabout homolog 3 precursor (Roundabout...	69	2e-11
<input type="checkbox"/>	tr	Q68DA2	_HUMAN Putative uncharacterized protein DKFPz781D102 [D...	69	2e-11
<input type="checkbox"/>	tr	Q59GD0	_HUMAN Polo-like kinase variant (Fragment) [Homo sapien...	69	2e-11
<input type="checkbox"/>	tr	Q3KPG9	_HUMAN V-mos Moloney murine sarcoma viral oncogene homo...	69	2e-11
<input type="checkbox"/>	sp_vs	Q8WX93-2	Isoform 2 of Q8WX93 - Homo sapiens (Human) [PALLD...	69	2e-11
<input type="checkbox"/>	sp_vs	Q96MS0-2	Isoform 2 of Q96MS0 - Homo sapiens (Human) [ROBO3...	69	2e-11
<input type="checkbox"/>	sp	Q8WX93	PALLD_HUMAN Palladin (Sarcoma antigen NY-SAR-77) (SIH0...	69	3e-11
<input type="checkbox"/>	sp	P45985	MP2K4_HUMAN Dual specificity mitogen-activated protein...	69	3e-11
<input type="checkbox"/>	sp	P00540	MOS_HUMAN Proto-oncogene serine/threonine-protein kina...	69	3e-11
<input type="checkbox"/>	sp	Q8IU85	KCC1D_HUMAN Calcium/calmodulin-dependent protein kinas...	69	3e-11
<input type="checkbox"/>	sp	O43293	DAPK3_HUMAN Death-associated protein kinase 3 (EC 2.7....	69	3e-11
<input type="checkbox"/>	sp	Q9Y243	AKT3_HUMAN RAC-gamma serine/threonine-protein kinase (...	69	3e-11
<input type="checkbox"/>	tr	Q9BWF9	_HUMAN PCTK3 protein (Fragment) [PCTK3] [Homo sapiens (...]	69	3e-11

<input type="checkbox"/>	tr	Q86X47	_HUMAN Neural cell adhesion molecule 1 [NCAM1] [Homo sa...	69 3e-11
<input type="checkbox"/>	tr	Q6PIE6	_HUMAN Mitogen-activated protein kinase kinase 4 [MAP2K...	69 3e-11
<input type="checkbox"/>	tr	Q6FHX4	_HUMAN MAP2K4 protein [MAP2K4] [Homo sapiens (Human)]	69 3e-11
<input type="checkbox"/>	tr	Q5VTI2	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	69 3e-11
<input type="checkbox"/>	tr	Q5VTI1	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	69 3e-11
<input type="checkbox"/>	tr	Q5SQQ7	_HUMAN Calcium/calmodulin-dependent protein kinase ID (...	69 3e-11
<input type="checkbox"/>	tr	Q56A86	_HUMAN AKT3 protein (Fragment) [AKT3] [Homo sapiens (Hu...	69 3e-11
<input type="checkbox"/>	tr	A1A4C4	_HUMAN Mitogen-activated protein kinase 4 [MAPK4] [Homo...	69 3e-11
<input type="checkbox"/>	sp_vs	Q9Y243-2	Isoform 2 of Q9Y243 - Homo sapiens (Human) [AKT3]...	69 3e-11
<input type="checkbox"/>	sp_vs	Q8IU85-2	Isoform 2 of Q8IU85 - Homo sapiens (Human) [CAMK1...	69 3e-11
<input type="checkbox"/>	sp_vs	Q8WX93-3	Isoform 3 of Q8WX93 - Homo sapiens (Human) [PALLD...	69 3e-11
<input type="checkbox"/>	sp_vs	Q8WX93-4	Isoform 4 of Q8WX93 - Homo sapiens (Human) [PALLD...	69 3e-11
<input type="checkbox"/>	sp_vs	Q8WX93-5	Isoform 5 of Q8WX93 - Homo sapiens (Human) [PALLD...	69 3e-11
<input type="checkbox"/>	sp	Q00141	SGK1_HUMAN Serine/threonine-protein kinase Sgk1 (EC 2....	69 4e-11
<input type="checkbox"/>	sp	P53778	MK12_HUMAN Mitogen-activated protein kinase 12 (EC 2.7...	69 4e-11
<input type="checkbox"/>	sp	P31152	MK04_HUMAN Mitogen-activated protein kinase 4 (EC 2.7....	69 4e-11
<input type="checkbox"/>	sp	Q9Y2U5	M3K2_HUMAN Mitogen-activated protein kinase kinase kin...	69 4e-11
<input type="checkbox"/>	sp	Q96RR4	KKCC2_HUMAN Calcium/calmodulin-dependent protein kinas...	69 4e-11
<input type="checkbox"/>	sp	Q8IWQ3	BRSK2_HUMAN BR serine/threonine-protein kinase 2 (EC 2...	69 4e-11
<input type="checkbox"/>	tr	Q6LC83	_HUMAN Cyclin dependent protein kinase (Cyclin-dependen...	69 4e-11
<input type="checkbox"/>	tr	Q5VY65	_HUMAN Serum/glucocorticoid regulated kinase [SGK] [Hom...	69 4e-11
<input type="checkbox"/>	tr	Q5TCN4	_HUMAN Serum/glucocorticoid regulated kinase [SGK] [Hom...	69 4e-11
<input type="checkbox"/>	tr	Q5TCN2	_HUMAN Serum/glucocorticoid regulated kinase (Serum/glu...	69 4e-11
<input type="checkbox"/>	tr	Q0VG04	_HUMAN Mitogen-activated protein kinase 4 (Mitogen-acti...	69 4e-11
<input type="checkbox"/>	tr	A5PKY1	_HUMAN TAO kinase 2 [TAOK2] [Homo sapiens (Human)]	69 4e-11
<input type="checkbox"/>	sp_vs	Q8TDC3-2	Isoform 2 of Q8TDC3 - Homo sapiens (Human) [BRSK1...	69 4e-11
<input type="checkbox"/>	sp_vs	Q8IWQ3-2	Isoform 2 of Q8IWQ3 - Homo sapiens (Human) [BRSK2...	69 4e-11
<input type="checkbox"/>	sp_vs	Q8IWQ3-3	Isoform 3 of Q8IWQ3 - Homo sapiens (Human) [BRSK2...	69 4e-11
<input type="checkbox"/>	sp_vs	Q8IWQ3-4	Isoform 4 of Q8IWQ3 - Homo sapiens (Human) [BRSK2...	69 4e-11
<input type="checkbox"/>	sp_vs	Q8IWQ3-5	Isoform 5 of Q8IWQ3 - Homo sapiens (Human) [BRSK2...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-2	Isoform 2 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-3	Isoform 3 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-4	Isoform 4 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-5	Isoform 5 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-6	Isoform 6 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q96RR4-7	Isoform 7 of Q96RR4 - Homo sapiens (Human) [CAMKK...	69 4e-11
<input type="checkbox"/>	sp_vs	Q8WX93-7	Isoform 7 of Q8WX93 - Homo sapiens (Human) [PALLD...	69 4e-11
<input type="checkbox"/>	sp	Q96NX5	KCC1G_HUMAN Calcium/calmodulin-dependent protein kinas...	68 5e-11
<input type="checkbox"/>	sp	Q8TDC3	BRSK1_HUMAN BR serine/threonine-protein kinase 1 (EC 2...	68 5e-11
<input type="checkbox"/>	tr	Q86VY5	_HUMAN MYO3A protein [MYO3A] [Homo sapiens (Human)]	68 5e-11
<input type="checkbox"/>	tr	Q69YJ3	_HUMAN Putative uncharacterized protein DKFZp762L185 (F...	68 5e-11
<input type="checkbox"/>	tr	Q15457	_HUMAN Protein-tyrosine kinase (Fragment) [Homo sapiens...	68 5e-11
<input type="checkbox"/>	tr	A2A344	_HUMAN ADAMTS-like 1 [ADAMTSL1] [Homo sapiens (Human)]	68 5e-11
<input type="checkbox"/>	sp_vs	Q96NX5-2	Isoform 2 of Q96NX5 - Homo sapiens (Human) [CAMK1...	68 5e-11
<input type="checkbox"/>	sp_vs	Q15746-3	Isoform 3A of Q15746 - Homo sapiens (Human) [MYLK...	68 5e-11
<input type="checkbox"/>	sp_vs	Q15746-4	Isoform 3B of Q15746 - Homo sapiens (Human) [MYLK...	68 5e-11
<input type="checkbox"/>	sp	Q9UBE8	NLK_HUMAN Serine/threonine kinase NLK (EC 2.7.11.24) (...	68 6e-11
<input type="checkbox"/>	sp	Q9H1R3	MYLK2_HUMAN Myosin light chain kinase 2, skeletal/card...	68 6e-11
<input type="checkbox"/>	sp	Q96JA1	LRIG1_HUMAN Leucine-rich repeats and immunoglobulin-li...	68 6e-11
<input type="checkbox"/>	sp	Q96QS6	KPSH2_HUMAN Serine/threonine-protein kinase H2 (EC 2.7...	68 6e-11
<input type="checkbox"/>	sp	P14619	KGP1B_HUMAN cGMP-dependent protein kinase 1, beta isoz...	68 6e-11
<input type="checkbox"/>	sp	Q13976	KGP1A_HUMAN cGMP-dependent protein kinase 1, alpha iso...	68 6e-11
<input type="checkbox"/>	sp	P19525	E2AK2_HUMAN Interferon-induced, double-stranded RNA-ac...	68 6e-11
<input type="checkbox"/>	tr	Q9BXC3	_HUMAN Serine/threonine protein kinase MST4a (Mst3 and ...	68 6e-11
<input type="checkbox"/>	tr	Q8IW76	_HUMAN EIF2AK2 protein (Fragment) [EIF2AK2] [Homo sapie...	68 6e-11
<input type="checkbox"/>	tr	Q7Z6F6	_HUMAN Interferon-inducible double-stranded RNA-depende...	68 6e-11
<input type="checkbox"/>	tr	Q6E0B2	_HUMAN Small intestine SPAK-like kinase [Homo sapiens (...	68 6e-11
<input type="checkbox"/>	tr	Q5XWD3	_HUMAN Leucine-rich repeat protein LRIG1 [LRIG1] [Homo ...	68 6e-11
<input type="checkbox"/>	tr	Q5SQU3	_HUMAN Protein kinase, cGMP-dependent, type I [PRKG1] [...	68 6e-11
<input type="checkbox"/>	sp_vs	P11362-17	Isoform 3 of P11362 - Homo sapiens (Human) [FGFR...	68 6e-11
<input type="checkbox"/>	sp	P37173	TGFR2_HUMAN TGF-beta receptor type-2 precursor (EC 2.7...	67 8e-11
<input type="checkbox"/>	sp	Q9UBF9	MYOTI_HUMAN Myotilin (Titin immunoglobulin domain prot...	67 8e-11
<input type="checkbox"/>	sp	Q13163	MP2K5_HUMAN Dual specificity mitogen-activated protein...	67 8e-11
<input type="checkbox"/>	sp	P53355	DAPK1_HUMAN Death-associated protein kinase 1 (EC 2.7....	67 8e-11
<input type="checkbox"/>	sp	Q12860	CNTN1_HUMAN Contactin-1 precursor (Neural cell surface...	67 8e-11
<input type="checkbox"/>	sp	Q9UQ88	CD2L2_HUMAN PITSLRE serine/threonine-protein kinase CD...	67 8e-11

<input type="checkbox"/>	sp	O00238	BMR1B_HUMAN Bone morphogenetic protein receptor type I...	67	8e-11
<input type="checkbox"/>	tr	Q96CA8	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	67	8e-11
<input type="checkbox"/>	tr	Q5VTK1	_HUMAN Death-associated protein kinase 1 [DAPK1] [Homo ...	67	8e-11
<input type="checkbox"/>	tr	Q5QPR4	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q5QPR3	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q59H88	_HUMAN Putative uncharacterized protein (Fragment) [Hom...	67	8e-11
<input type="checkbox"/>	tr	Q53EZ9	_HUMAN Mitogen-activated protein kinase kinase 3 isoform...	67	8e-11
<input type="checkbox"/>	tr	Q4VBY6	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	67	8e-11
<input type="checkbox"/>	tr	Q2TAJ0	_HUMAN Cell division cycle 2-like 2 (PITSLRE proteins) ...	67	8e-11
<input type="checkbox"/>	tr	Q1W5W0	_HUMAN Death-associated protein kinase 1 (Death-associa...	67	8e-11
<input type="checkbox"/>	tr	Q14CQ7	_HUMAN Death-associated protein kinase 1 [DAPK1] [Homo ...	67	8e-11
<input type="checkbox"/>	tr	Q0VAA6	_HUMAN V-akt murine thymoma viral oncogene homolog 3 (P...	67	8e-11
<input type="checkbox"/>	tr	A3QNQ0	_HUMAN Transforming growth factor beta receptor II (Tra...	67	8e-11
<input type="checkbox"/>	tr	AL14K2	_HUMAN Mitogen-activated protein kinase 8 (Mitogen-acti...	67	8e-11
<input type="checkbox"/>	tr	ALKZ92	_HUMAN Cardiac peroxidase [Homo sapiens (Human)]	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-2	Isoform SV1 of Q9UQ88 - Homo sapiens (Human) [CDC...	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-3	Isoform SV2 of Q9UQ88 - Homo sapiens (Human) [CDC...	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-4	Isoform SV3 of Q9UQ88 - Homo sapiens (Human) [CDC...	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-5	Isoform SV7 of Q9UQ88 - Homo sapiens (Human) [CDC...	67	8e-11
<input type="checkbox"/>	sp_vs	Q9UQ88-10	Isoform 4 of Q9UQ88 - Homo sapiens (Human) [CDC2...	67	8e-11
<input type="checkbox"/>	sp_vs	Q12860-2	Isoform 2 of Q12860 - Homo sapiens (Human) [CNTN1...	67	8e-11
<input type="checkbox"/>	sp_vs	Q12860-3	Isoform 3 of Q12860 - Homo sapiens (Human) [CNTN1...	67	8e-11
<input type="checkbox"/>	sp_vs	P45983-3	Isoform 3 of P45983 - Homo sapiens (Human) [MAPK8...	67	8e-11
<input type="checkbox"/>	sp_vs	P45983-4	Isoform 4 of P45983 - Homo sapiens (Human) [MAPK8...	67	8e-11
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<input type="checkbox"/>	sp	Q86SG6	NEK8_HUMAN Serine/threonine-protein kinase Nek8 (EC 2....	67	1e-10
<input type="checkbox"/>	sp	P46734	MP2K3_HUMAN Dual specificity mitogen-activated protein...	67	1e-10
<input type="checkbox"/>	sp	Q16659	MK06_HUMAN Mitogen-activated protein kinase 6 (EC 2.7....	67	1e-10
<input type="checkbox"/>	sp	Q13237	KGP2_HUMAN cGMP-dependent protein kinase 2 (EC 2.7.11....	67	1e-10
<input type="checkbox"/>	sp	Q6WRI0	IGS10_HUMAN Immunoglobulin superfamily member 10 precu...	67	1e-10
<input type="checkbox"/>	sp	O14757	CHK1_HUMAN Serine/threonine-protein kinase Chk1 (EC 2....	67	1e-10
<input type="checkbox"/>	tr	Q6FI23	_HUMAN MAP2K3 protein [MAP2K3] [Homo sapiens (Human)]	67	1e-10
<input type="checkbox"/>	tr	Q6PHG1	_HUMAN MAP2K3 protein (Fragment) [MAP2K3] [Homo sapiens...	67	1e-10
<input type="checkbox"/>	tr	Q68DY3	_HUMAN Putative uncharacterized protein DKFZp686P2031 [...	67	1e-10
<input type="checkbox"/>	tr	A6NIC5	_HUMAN Uncharacterized protein NEK8 [NEK8] [Homo sapien...	67	1e-10
<input type="checkbox"/>	sp_vs	Q8TD08-3	Isoform 3 of Q8TD08 - Homo sapiens (Human) [MAPK1...	67	1e-10
<input type="checkbox"/>	sp_vs	P46734-2	Isoform 1 of P46734 - Homo sapiens (Human) [MAP2K...	67	1e-10
<input type="checkbox"/>	sp_vs	P46734-3	Isoform 2 of P46734 - Homo sapiens (Human) [MAP2K...	67	1e-10
<input type="checkbox"/>	sp_vs	Q15746-5	Isoform 4 of Q15746 - Homo sapiens (Human) [MYLK]...	67	1e-10
<input type="checkbox"/>	sp	Q8TD08	MK15_HUMAN Mitogen-activated protein kinase 15 (EC 2.7...	67	1e-10
<input type="checkbox"/>	sp	Q9UIK4	DAPK2_HUMAN Death-associated protein kinase 2 (EC 2.7....	67	1e-10
<input type="checkbox"/>	sp	P37023	ACV1L1_HUMAN Serine/threonine-protein kinase receptor R...	67	1e-10
<input type="checkbox"/>	tr	A6NGA8	_HUMAN Uncharacterized protein ACVRL1 [ACVRL1] [Homo sa...	67	1e-10
<input type="checkbox"/>	sp	P36897	TGFR1_HUMAN TGF-beta receptor type-1 precursor (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	Q86YV6	SGK85_HUMAN Uncharacterized serine/threonine-protein k...	66	2e-10
<input type="checkbox"/>	sp	P53779	MK10_HUMAN Mitogen-activated protein kinase 10 (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	Q9UBS0	KS6B2_HUMAN Ribosomal protein S6 kinase beta-2 (EC 2.7...	66	2e-10
<input type="checkbox"/>	sp	P31749	AKT1_HUMAN RAC-alpha serine/threonine-protein kinase (...	66	2e-10
<input type="checkbox"/>	tr	Q9BRS0	_HUMAN Ribosomal protein S6 kinase, 70kDa, polypeptide ...	66	2e-10
<input type="checkbox"/>	tr	Q6F9H2	_HUMAN Mitogen-activated protein kinase kinase 4 [MAP2K...	66	2e-10
<input type="checkbox"/>	tr	Q6IR47	_HUMAN TGFR1 protein [TGFR1] [Homo sapiens (Human)]	66	2e-10
<input type="checkbox"/>	tr	Q5T7S2	_HUMAN Transforming growth factor, beta receptor I (Act...	66	2e-10
<input type="checkbox"/>	tr	A6NG28	_HUMAN Uncharacterized protein MAPK10 [MAPK10] [Homo sa...	66	2e-10
<input type="checkbox"/>	sp_vs	P53779-2	Isoform Alpha-1 of P53779 - Homo sapiens (Human) ...	66	2e-10
<input type="checkbox"/>	sp	Q96RG2	PASK_HUMAN PAS domain-containing serine/threonine-prot...	66	2e-10
<input type="checkbox"/>	sp	P27361	MK03_HUMAN Mitogen-activated protein kinase 3 (EC 2.7....	66	2e-10
<input type="checkbox"/>	sp	P21127	CD2L1_HUMAN PITSLRE serine/threonine-protein kinase CD...	66	2e-10
<input type="checkbox"/>	sp	P31751	AKT2_HUMAN RAC-beta serine/threonine-protein kinase (E...	66	2e-10
<input type="checkbox"/>	tr	Q6P5Y5	_HUMAN CDC2L2 protein (Fragment) [CDC2L2] [Homo sapiens...	66	2e-10
<input type="checkbox"/>	tr	Q6FG83	_HUMAN STK17B protein (Fragment) [STK17B] [Homo sapiens...	66	2e-10
<input type="checkbox"/>	tr	A5YM56	_HUMAN PRKG1 protein [PRKG1] [Homo sapiens (Human)]	66	2e-10
<input type="checkbox"/>	tr	A4VC15	_HUMAN CDC2L1 protein (Fragment) [CDC2L1] [Homo sapiens...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-2	Isoform SV1 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-3	Isoform 2 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-4	Isoform 3 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-5	Isoform SV4 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10

<input type="checkbox"/>	sp_vs	P21127-6	Isoform SV5 of P21127 - Homo sapiens (Human) [CDC...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-8	Isoform 8 of P21127 - Homo sapiens (Human) [CDC2L...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-9	Isoform SV10 of P21127 - Homo sapiens (Human) [CD...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-10	Isoform SV11 of P21127 - Homo sapiens (Human) [C...	66	2e-10
<input type="checkbox"/>	sp_vs	P21127-12	Isoform 7 of P21127 - Homo sapiens (Human) [CDC2...	66	2e-10
<input type="checkbox"/>	sp_vs	Q96RG2-2	Isoform 2 of Q96RG2 - Homo sapiens (Human) [PASK]...	66	2e-10
<input type="checkbox"/>	sp_vs	O15530-3	Isoform 3 of O15530 - Homo sapiens (Human) [PDPK1...	66	2e-10
<input type="checkbox"/>	sp	O43930	PRKY_HUMAN Serine/threonine-protein kinase PRKY (EC 2...	65	3e-10
<input type="checkbox"/>	sp	P98160	PGBM_HUMAN Basement membrane-specific heparan sulfate ...	65	3e-10
<input type="checkbox"/>	sp	Q38SD2	LRRK1_HUMAN Leucine-rich repeat serine/threonine-prote...	65	3e-10
<input type="checkbox"/>	sp	P24723	KPCL_HUMAN Protein kinase C eta type (EC 2.7.11.13) (n...	65	3e-10
<input type="checkbox"/>	sp	Q8N5S9	KKCC1_HUMAN Calcium/calmodulin-dependent protein kinas...	65	3e-10
<input type="checkbox"/>	sp	Q04771	ACVR1_HUMAN Activin receptor type-1 precursor (EC 2.7....	65	3e-10
<input type="checkbox"/>	tr	Q8NE03	_HUMAN Protein kinase C, eta (Protein kinase C, eta, is...	65	3e-10
<input type="checkbox"/>	tr	Q5VU27	_HUMAN Heparan sulfate proteoglycan 2 [HSPG2] [Homo sap...	65	3e-10
<input type="checkbox"/>	tr	A8CZ58	_HUMAN Extracellular signal-regulated kinase-1 splice v...	65	3e-10
<input type="checkbox"/>	tr	A6NDF7	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65	3e-10
<input type="checkbox"/>	tr	A6H8V9	_HUMAN LRRK1 protein (Fragment) [LRRK1] [Homo sapiens (...	65	3e-10
<input type="checkbox"/>	sp_vs	Q38SD2-3	Isoform 3 of Q38SD2 - Homo sapiens (Human) [LRRK1...	65	3e-10
<input type="checkbox"/>	sp	O94768	ST17B_HUMAN Serine/threonine-protein kinase 17B (EC 2....	65	4e-10
<input type="checkbox"/>	sp	C14976	GAK_HUMAN Cyclin G-associated kinase (EC 2.7.11.1) [GA...	65	4e-10
<input type="checkbox"/>	tr	Q6FG98	_HUMAN STK17B protein [STK17B] [Homo sapiens (Human)]	65	4e-10
<input type="checkbox"/>	tr	Q53QE7	_HUMAN Putative uncharacterized protein STK17B (Serine/...	65	4e-10
<input type="checkbox"/>	sp_vs	Q8TD08-2	Isoform 2 of Q8TD08 - Homo sapiens (Human) [MAPK1...	65	4e-10
<input type="checkbox"/>	sp	Q496M5	PLK5_HUMAN Serine/threonine-protein kinase PLK5 (EC 2....	65	5e-10
<input type="checkbox"/>	sp	Q92859	NEO1_HUMAN Neogenin precursor [NEO1] [Homo sapiens (Hu...	65	5e-10
<input type="checkbox"/>	sp	Q6P2M8	KCC1B_HUMAN Calcium/calmodulin-dependent protein kinas...	65	5e-10
<input type="checkbox"/>	sp	O15075	DCLK1_HUMAN Serine/threonine-protein kinase DCLK1 (EC ...	65	5e-10
<input type="checkbox"/>	tr	Q5VZZ1	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65	5e-10
<input type="checkbox"/>	tr	Q5VZZ0	_HUMAN Doublecortin and CaM kinase-like 1 (Doublecortin...	65	5e-10
<input type="checkbox"/>	tr	Q5VZY8	_HUMAN Doublecortin and CaM kinase-like 1 [DCAMKL1] [Ho...	65	5e-10
<input type="checkbox"/>	tr	Q3M994	_HUMAN Dominant-negative kinase-deficient Brutons tyros...	65	5e-10
<input type="checkbox"/>	tr	A6N135	_HUMAN Uncharacterized protein HSPG2 [HSPG2] [Homo sapi...	65	5e-10
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<input type="checkbox"/>	sp_vs	O15075-2	Isoform 1 of O15075 - Homo sapiens (Human) [DCLK1...	65	5e-10
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<input type="checkbox"/>	sp	Q32MK0	MYLK3_HUMAN Putative myosin light chain kinase 3 (EC 2...	64	7e-10
<input type="checkbox"/>	sp	Q13233	M3K1_HUMAN Mitogen-activated protein kinase kinase kin...	64	7e-10
<input type="checkbox"/>	sp	Q13555	KCC2G_HUMAN Calcium/calmodulin-dependent protein kinas...	64	7e-10
<input type="checkbox"/>	sp	P22612	KAPCG_HUMAN cAMP-dependent protein kinase, gamma-catal...	64	7e-10
<input type="checkbox"/>	sp	P36894	BMR1A_HUMAN Bone morphogenetic protein receptor type I...	64	7e-10
<input type="checkbox"/>	sp	P20594	ANPRB_HUMAN Atrial natriuretic peptide receptor B prec...	64	7e-10

Graphical overview of the alignments

[Click here](#)

to resubmit your query after masking regions matching PROSITE profiles or Pfam HMMs

(Help) (use ScanProsite for more details about PROSITE matches)

Profile hits

Pfam hits

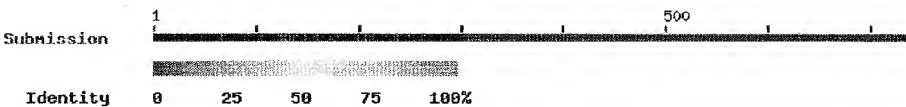
Matches on query sequence

Submission

Q5B1G2_HUMAN
P11362-14
P11362-3
P11362-4
P11362-7
P11362-5
P11362-5
P11362-6
P11362-3
P11362-3
P11362-18
P11362-18
P11362-5
P11362-16
P11362-20
P11362-9
P11362-9
P11362-10

Matches on hit sequences (sort scale)

1 100 200 300 500 1034



Alignments

tr Q5BJG2 Fibroblast growth factor receptor 1 (Fms-related tyrosine kinase 2, 731 AA
Q5BJG2_HUMAN Pfeiffer syndrome) [FGFR1] [Homo sapiens (Human)] align

Score = 1420 bits (3677), Expect = 0.0
Identities = 696/735 (94%), Positives = 709/735 (96%), Gaps = 6/735 (0%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDSSSEKETDNTKPNFV 60
MW WKCLLFWAVLVLTATLCTARP+PTLPEQDALPSSSEDDDDSSSEKETDNTKPNFV
Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDSSSEKETDNTKPNFV 60

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSSGTPNPTRLWLKNGKEFKPDHRIGGYKVRYA 120
APYWTSPKMEKKLHAVPAAKTVKFKCPSSSGTPNPTRLWLKNGKEFKPDHRIGGYKVRYA
Sbjct: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSSGTPNPTRLWLKNGKEFKPDHRIGGYKVRYA 120

Query: 121 TWSIIMDSVVPSSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGS 180
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Query: 181 NVEFMCKVYSDPPQPHIQWLKHEVNGSKIGPDNLPYVQILKHSINSSDAE--VLTLPNV 238
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Sbjct: 181 NVEFMCKVYSDPPQPHIQWLKHEVNGSKIGPDNLPYVQILKTAGVNTDKEMEVLHLRNV 240

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPPLYLEIIYYCTGAFLI 298
+ +GEY C N IG ++ SAWLTV +ALEERPAVMTSPPLYLEIIYYCTGAFLI
Sbjct: 241 SFEDAGEYTCLAGNSIGLSHSAWLTVL---EALERPAVMTSPPLYLEIIYYCTGAFLI 296

Query: 299 SCMLGSVVIYKMKSGTKKSDPHSQMAVHKLAISIPLRRQVTVSADSSASMSGVLLVRPS 358
MW WKCLLFWAVLVLTATLCTARP+PTLPEQDALPSSSEDDDDSSSEKETDNTKPNFV
Sbjct: 297 SCMLGSVVIYKMKSGTKKSDPHSQMAVHKLAISIPLRRQVTVSADSSASMSGVLLVRPS 356

Query: 359 RLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGBGCFQGVVLAFAIIGLDKDKPFR 418
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Sbjct: 357 RLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGBGCFQGVVLAFAIIGLDKDKPFR 416

Query: 419 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLEACTODGPLYVIVEYASKG 478
VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTODGPLYVIVEYASKG
Sbjct: 417 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTODGPLYVIVEYASKG 476

Query: 479 NLREYLQARRPPGLEIYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR 538
NLREYLQARRPPGLEIYCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR
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Query: 539 NVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVVSFG 598
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Query: 599 VLLWEIPTLGGSPYPGVVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTF 658
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Query: 659 KQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPFDPTRSSSTCSSGEDSVFSHEPLPEEPCL 718
KQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPFDPTRSSSTCSSGEDSVFSHEPLPEEPCL
Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPFDPTRSSSTCSSGEDSVFSHEPLPEEPCL 716

Query: 719 PRHPTQLANGGLKRR 733
 PRHP QLAN GLKRR
 Sbjct: 717 PRHPAQLANGGLKRR 731

sp_vs P11362-14 Isoform 15 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA
 FGFR1_HUMAN (Human)] align

Score = 1420 bits (3677), Expect = 0.0
 Identities = 696/735 (94%), Positives = 709/735 (96%), Gaps = 6/735 (0%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV 60
 MW WKCLLFWAVLVLTATLCTARPA+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNPV 60

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
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Query: 121 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS 180
 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS
 Sbjct: 121 TWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVALGS 180

Query: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSINSSDAE--VLTLFNV 238
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 Sbjct: 181 NVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLRNV 240

Query: 239 TEAQSGEYVCKVSNYIGEANSALVTVPVAKALEERPAVMTSPLYLEIIYYCTGAFLI 298
 + +GEY C N IG ++ SALT V +ALEERPAVMTSPLYLEIIYYCTGAFLI
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Query: 299 SCMLGSGVIYYKMKSGTKKSDFHSSQMAVHKLAKSIPLRRQVTVSADSSASMSNGVLLVRPS 358
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Query: 419 VTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKG 478
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Query: 479 NLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAAR 538
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Query: 539 NVLVTEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG 598
 NVLVTEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG
 Sbjct: 537 NVLVTEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFG 596

Query: 599 VLLWEIPTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTF 658
 VLLWEIPTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTF
 Sbjct: 597 VLLWEIPTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTF 656

Query: 659 KQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPFPDTRSSSTCSSGEDSVFSHEPLPEEPCL 718
 KQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPFPDTRSSSTCSSGEDSVFSHEPLPEEPCL
 Sbjct: 657 KQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPFPDTRSSSTCSSGEDSVFSHEPLPEEPCL 716

Query: 719 PRHPTQLANGGLKRR 733
 PRHP QLAN GLKRR
 Sbjct: 717 PRHPAQLANGGLKRR 731

sp_vs P11362-3 Isoform 6 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 733 AA
 FGFR1_HUMAN (Human)] align

Score = 1415 bits (3664), Expect = 0.0
 Identities = 696/737 (94%), Positives = 709/737 (96%), Gaps = 8/737 (1%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN-- 58
 MW WKCLLFWAVLVLTATLCTARPA+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
 PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
 Sbjct: 61 PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 178
 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL
 Sbjct: 121 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANKTVAL 180

```

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
          GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAF 296
          NV+ +GEY C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAMVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGSGVVIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
          LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416
          PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP
Sbjct: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYAS 476
          NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTQDGPLYVIVEYAS
Sbjct: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYAS 476

Query: 477 KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
          KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA
Sbjct: 477 KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA 536

Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596
          ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS
Sbjct: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

Query: 597 FGVLLWEIFTLGGSPPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
          FGVLLWEIFTLGGSPPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP
Sbjct: 597 FGVLLWEIFTLGGSPPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656

Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716
          TFKQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP
Sbjct: 657 TFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716

Query: 717 CLPRHPTQLANSGLKRR 733
          CLPRHP QLAN GLKRR
Sbjct: 717 CLPRHPAQLANGGLKRR 733

```

sp_vs P11362-4 Isoform 8 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 731 AA align
FGFR1_HUMAN (Human)]

Score = 1407 bits (3642), Expect = 0.0
Identities = 694/737 (94%), Positives = 707/737 (95%), Gaps = 10/737 (1%)

```

Query: 1 MWGKCKLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN-- 58
          MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN
Sbjct: 1 MWGKCKLLFWAVLVTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
          PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61 PVAPYWTSPKEKMKLLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRILQAGLPANKTVAL 178
          YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVPVSDKGNYSICIVENEYGSINHTYQLDVVERSHPHRILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
          GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAF 296
          NV+ +GEY C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALEERPAMVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCMGSGVVIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
          LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV TVSADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416
          PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP
Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYAS 476
          NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTQDGPLYVIVEYAS
Sbjct: 415 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
          KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA
Sbjct: 475 KGNLREYLQARRPPGLECYNPSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLA 534

Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWS 596

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          ARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWS
Sbjct: 535 ARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTTNGRLPVKWMPEALFDRIYTHQSDVWS 594

Query: 597 FGVLLWEIFTLGGSPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
          FGVLLWEIFTLGGSPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP
Sbjct: 595 FGVLLWEIFTLGGSPYPGVFVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 654

Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIFLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 716
          TFKQLVE LDRIVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP
Sbjct: 655 TFKQLVEDLDRIVALTSNQEYLDLSMPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEP 714

Query: 717 CLPRHPTQLANSGLKRR 733
          CLPRHP QLAN GLKRR
Sbjct: 715 CLPRHPAQLANGGLKRR 731

```

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sp_vs P11362-7      Isoform 14 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA
FGFR1_HUMAN      (Human)] align

```

Score = 1357 bits (3513), Expect = 0.0
Identities = 668/705 (94%), Positives = 680/705 (96%), Gaps = 6/705 (0%)

```

Query: 31  DALPSSDDDDDDSSSEEKTDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DALPSSDDDDDDSSSEEKTDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS
Sbjct: 120 DALPSSDDDDDDSSSEEKTDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 179

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
          GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVP SDKGNYTCIVENEYGSINH
Sbjct: 180 GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVP SDKGNYTCIVENEYGSINH 239

Query: 151 TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG
Sbjct: 240 TYQLDVVERSHPHPILOAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 299

Query: 211 PDNLPPYQILKHSGINSDDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANSALWTVTRP 268
          PDNLPPYQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 300 PDNLPPYQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSALWTVL-- 357

Query: 269 VAKALEERPAMVTSPLYLEIIYCTGAFLISCMGSGVVIYKMKSGTKKSDFHSMQMAVHKL 328
          +ALEERPAMVTSPLYLEIIYCTGAFLISCM+GSGVI+YKMKSGTKKSDFHSMQMAVHKL
Sbjct: 358 --EALERPAVMTSPLYLEIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSMQMAVHKL 415

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 388
          AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR
Sbjct: 416 AKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 475

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM
Sbjct: 476 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 535

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS
Sbjct: 536 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 595

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT 568
          KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT
Sbjct: 596 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMVKIADFGGLARDIHHIDYKKTT 655

Query: 569 TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVFVEELFKLLKEGH 628
          TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVFVEELFKLLKEGH
Sbjct: 656 TNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVFVEELFKLLKEGH 715

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEVLDRIVALTSNQEYLDLSIFLDQYS 688
          RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVE LDRIVALTSNQEYLDLS+PLDQYS
Sbjct: 716 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYS 775

Query: 689 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
          PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 776 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

```

Score = 91.3 bits (225), Expect = 5e-18
Identities = 78/305 (25%), Positives = 118/305 (38%), Gaps = 81/305 (26%)

```

Query: 1  MWGWKCLLFWAVLVATLCTARPAPTLPEQDALPSSDDDDDDSSSEEKTDNTKPNVP 60
          MW WKCLLFWAVLVATLCTARPA+PTLPEQ
Sbjct: 1  MWSWKCLLFWAVLVATLCTARPSPTLPEQ----- 30

Query: 61  APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
          A W +P ++E L V ++ +C ++ WL++G + +R R
Sbjct: 31  AQPNGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINH TYQLDVVERSHPH----- 162
          + + VP+D G Y C+ + GS + ++V + P
Sbjct: 83  GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEEKTD 142

```


Query: 163 ----RPILQAGLPANK-----TVALGSNVEFMCKVYSDPQPPIQWLKHIEVNGSKIGPD 212
 P+ K V V+F C P P ++WLK NG + PD
 Sbjct: 143 NTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPD 198

Query: 213 NLPYVQILKHSGINSDDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT-----R 267
 + ++++ + + + +V + G Y C V N G N + L V R
 Sbjct: 199 HRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVERSHPH 252

Query: 268 PVAKA 272
 P+ +A
 Sbjct: 253 PILQA 257

sp P11362 Basic fibroblast growth factor receptor 1 precursor (EC 2.7.10.1) 822 AA
 FGFR1_HUMAN (FGFR-1) (bFGF-R) (Fms-like tyrosine kinase 2) (c-fgr) align
 (CD331 antigen) [FGFR1] [Homo sapiens (Human)]

Score = 1352 bits (3500), Expect = 0.0
 Identities = 668/707 (94%), Positives = 680/707 (96%), Gaps = 8/707 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 148
 SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI
 Sbjct: 180 SSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVERSHPHPIAQGLPANKTVALGSNVEFMCKVYSDPQPPIQWLKHIEVNGSK 208
 NHTYQLDVERSHPHPIAQGLPANKTVALGSNVEFMCKVYSDPQPPIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVERSHPHPIAQGLPANKTVALGSNVEFMCKVYSDPQPPIQWLKHIEVNGSK 299

Query: 209 IGPDLNLPYVQILKHSGINSDDAE--VLTILFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL 359

Query: 267 RPVAKALEERPAMVTSPLYLEIIYCTGAFLISCMGSGVIYKMKSGTKKSDPHSQMAVH 326
 +ALEERPAMVTSPLYLEIIYCTGAFLISCM+GSGVIYKMKSGTKKSDPHSQMAVH
 Sbjct: 360 ----EALERPAMVTSPLYLEIIYCTGAFLISCMGSGVIYKMKSGTKKSDPHSQMAVH 415

Query: 327 KLAISIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAISIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAISIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 475

Query: 387 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
 Sbjct: 476 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 535

Query: 447 KMIGKHKNIINLLACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL 506
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL
 Sbjct: 536 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEQL 595

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 566
 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK
 Sbjct: 596 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 655

Query: 567 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGSPYPGPVPEELFKLLKE 626
 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGSPYPGPVPEELFKLLKE
 Sbjct: 656 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFTLGSPYPGPVPEELFKLLKE 715

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ
 Sbjct: 716 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 775

Query: 687 YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
 YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP QLANS GLKRR
 Sbjct: 776 YSPSFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 822

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60
 MW WKCLLFWAVLVLTATLCTARP+PTLPEQ
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVERS----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETD 142

```

Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          P+          K          V          V+F C          P P ++WLK          NG +
Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFK 198

Query: 211 PDNLPPYQILKHSGINSDDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT---- 266
          PD+          +++++          + + +V +          G Y C V N          G N +          L V
Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
          RP+ +A
Sbjct: 253 HRPILQA 259

```

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tr Q53H63      Fibroblast growth factor receptor 1 isoform 2 variant (Fragment) 820 AA
Q53H63_HUMAN  [Homo sapiens (Human)] align

```

Score = 1351 bits (3496), Expect = 0.0
 Identities = 665/705 (94%), Positives = 678/705 (96%), Gaps = 6/705 (0%)

```

Query: 31  DALPSSSEDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
          DALPSSSEDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS
Sbjct: 120 DALPSSSEDDDDDDSSSEKETDNTKPNFVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 179

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
          GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP  DKGNYTCIVENEYGSINH
Sbjct: 180 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 239

Query: 151 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG
Sbjct: 240 TYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 299

Query: 211 PDNLPPYQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
          PDNLPPYQILK +G+N++D E  VL L NV+  +GEY C  N IG ++ SAWLTV
Sbjct: 300 PDNLPPYQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSWLTVL-- 357

Query: 269 VAKALEERPAVMTSPLYLEII IYCTGAPLISCMGSVIIYKMKSGTKKSDFHQSQMAVHKL 328
          +ALEERPAVMTSPLYLEII IYCTGAPLISCM+GSVI+YKMKSGTKKSDFHQSQMAVHKL
Sbjct: 358 --BALEERPAVMTSPLYLEII IYCTGAPLISCMVGSVIVYKMKSGTKKSDFHQSQMAVHKL 415

Query: 329 AKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 388
          AKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR
Sbjct: 416 AKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDR 475

Query: 389 LVLGKPLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          LVLG+PLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM
Sbjct: 476 LVLGRPLGEGCFGQVVLAEAI GLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 535

Query: 449 IGKHKNI INLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
          IGKHKNI INLL ACTQDGPLYVIVEYASKGNLREYLQA RPPGLECYNPSHNPEEQQLSS
Sbjct: 536 IGKHKNI INLLGACTQDGPLYVIVEYASKGNLREYLQAWRPPGLECYNPSHNPEEQQLSS 595

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGLARDIHHIDYYKKT 568
          KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGLARDIHHIDYYKKT
Sbjct: 596 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGLARDIHHIDYYKKT 655

Query: 569 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH
Sbjct: 656 TNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 715

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
          RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQYS
Sbjct: 716 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQYS 775

Query: 689 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
          PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 776 PSFPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

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Score = 90.1 bits (222), Expect = 1e-17
 Identities = 78/305 (25%), Positives = 117/305 (38%), Gaps = 81/305 (26%)

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Query: 1  MWGKCLLFWAVLVTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNFV 60
          MW WKCLLFWAVLVTATLCTARP+PTLPEQ
Sbjct: 1  MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30

Query: 61  APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
          A W +P ++E L V          ++ +C          ++ WL++G +          +R          R
Sbjct: 31  AQPWGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERSPH----- 162
          + +          VP+D G Y C+ +          GS          + ++V +          P
Sbjct: 83  GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSSEDDDDDDSSSEKETD 142

Query: 163 ----RPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
          P+          K          V          V+F C          P P ++WLK          NG +          PD

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Sbjct: 143 NTKPNPVAPYWTSSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPD 198

Query: 213 NLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT-----R 267
      +      +++++ +      + + +V      G Y C V N G N + L V      R
Sbjct: 199 HRIGGYKVRATWS-----IIMDSVVPFDKGNVTCIVENEYGSINHTYQLDVVERSPHR 252

Query: 268 PVAKA 272
      P+ +A
Sbjct: 253 PILQA 257

tr Q59H40      Fibroblast growth factor receptor 1 isoform 1 variant (Fragment) 814 AA
Q59H40_HUMAN  [Homo sapiens (Human)] align

Score = 1344 bits (3478), Expect = 0.0
Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPN--PVAPYWTSSPEKMEKKLHAVPAAKTVKFKCP 88
      DALPSSDDDDDDSSSEKETDNTKPN PVAPYWTSSPEKMEKKLHAVPAAKTVKFKCP
Sbjct: 114 DALPSSDDDDDDSSSEKETDNTKPNRMPVAPYWTSSPEKMEKKLHAVPAAKTVKFKCP 173

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNVTCIVENEYGSI 148
      SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNVTCIVENEYGSI
Sbjct: 174 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNVTCIVENEYGSI 233

Query: 149 NHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
      NHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
Sbjct: 234 NHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 293

Query: 209 IGPDLNLPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
      IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
Sbjct: 294 IGPDLNLPYVQILKTACVNTTDKEMEVLHLRNVSPEDAGEYTCLAGNSIGLSHHSAWLTVL 353

Query: 267 RPVAKALEERPFAVMTSPLYLEIIIIYCTGAFLISCMGSVIIYKMKSGTKKSDFHSQMAVH 326
      +ALEERPFAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVH
Sbjct: 354 ----EALERPFAVMTSPLYLEIIIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVH 409

Query: 327 KLAKSIPLRQVTVSADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
      KLAKSIPLRQV SADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
Sbjct: 410 KLAKSIPLRQV--SADSSASMSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 467

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
Sbjct: 468 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 527

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ
Sbjct: 528 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 587

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 566
      SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK
Sbjct: 588 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 647

Query: 567 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIPTLGGSPYPGVPEELFKLLKE 626
      KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIPTLGGSPYPGVPEELFKLLKE
Sbjct: 648 KTTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIPTLGGSPYPGVPEELFKLLKE 707

Query: 627 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
      GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVE LDRIVALTSNQEYLDLS+PLDQ
Sbjct: 708 GHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQ 767

Query: 687 YSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHPTQLANGSLKRR 733
      YSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHP QLAN GLKRR
Sbjct: 768 YSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHPAQLANGSLKRR 814

Score = 43.1 bits (100), Expect = 0.002
Identities = 49/244 (20%), Positives = 88/244 (36%), Gaps = 53/244 (21%)

Query: 64 WTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWS 123
      W +P ++E L V ++ +C ++ WL++G + +R R
Sbjct: 28 WGAPVEVESFL--VHPGDLQLRCLRDDVQ-SINWLRDGVQLAESNR-----TRITGEE 79

Query: 124 IIMDSVVPSPDKGNVTCIVENEYGSINHTYQLDVVERSP----- 161
      + + VP+D G Y C+ + GS + ++V + P
Sbjct: 80 VEQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETDNTK 139

Query: 162 --HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
      P+ K V V+F C P P ++WLK NG + PD+
Sbjct: 140 PNRMPVAPYWTSSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFKPDH 195

Query: 214 LPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT-----RP 268
      +++++ + + + +V + G Y C V N G N + L V RP
Sbjct: 196 RIGGYKVRATWS-----IIMDSVVPSPDKGNVTCIVENEYGSINHTYQLDVVERSPHRP 249

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Query: 269 VAKA 272
 + +A
 Sbjct: 250 ILQA 253

sp_vs P11362-2 Isoform 4 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 820 AA
 FGFR1_HUMAN (Human)] align

Score = 1344 bits (3478), Expect = 0.0
 Identities = 666/707 (94%), Positives = 678/707 (95%), Gaps = 10/707 (1%)

Query: 31 DALPSSDDDDDDSSSEEEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSDDDDDDSSSEEEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSDDDDDDSSSEEEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 148
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDNLPYVQILKESGINSSDAE--VLTFLNVTEAQSCYVCKVSNYIGEANQSAWLTVT 266
 IGPDNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDNLPYVQILKTAGVTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHSAWLTVL 359

Query: 267 RPAKALEERPAMVMTSPYLEII IYCTGAFLISCMGSLVIYKMKSGTKKSDPHSQMAVH 326
 +ALEERPAMVMTSPYLEII IYCTGAFLISCM+GSVI+YKMKSGTKKSDPHSQMAVH
 Sbjct: 360 ----EALERPAMVMTSPYLEII IYCTGAFLISCMVGSVIVYKMKSGTKKSDPHSQMAVH 415

Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAKSIPLRQV SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAKSIPLRQV--SADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 473

Query: 387 DRVLVGLKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLI SEMEMM 446
 DRVLVGLKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLI SEMEMM
 Sbjct: 474 DRVLVGLKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLI SEMEMM 533

Query: 447 KMIGKHKNIINLL EACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCYNPSHNPEEQ 506
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCYNPSHNPEEQ
 Sbjct: 534 KMIGKHKNIINLL EACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYCYNPSHNPEEQ 593

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 566
 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK
 Sbjct: 594 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADPGLARDIHHIDYK 653

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 626
 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE
 Sbjct: 654 KTTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPEELFKLLKE 713

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRI VALTSNQEYLDLSIPLDQ 686
 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRIVALT SNQEYLDLS+PLDQ
 Sbjct: 714 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALT SNQEYLDLSMPLDQ 773

Query: 687 YSPSPDTRSTCSGSDSVFSHEPLPEEPCLPRHPTQLANSGLKRR 733
 YSPSPDTRSTCSGSDSVFSHEPLPEEPCLPRHP QLAN GLKRR
 Sbjct: 774 YSPSPDTRSTCSGSDSVFSHEPLPEEPCLPRHPAQLANGGLKRR 820

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGKCLLFWAVLVTATLCTARPAITLPEQDALPSSDDDDDDSSSEEEKETDNTKPNPV 60
 MW WKCLLFWAVLVTATLCTARP+PTLPEQ
 Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 AQPWGAPEVESFL--VHPGDLQLRCRLRDDVQ--SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEEEKETD 142

Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 P+ K V V+FC P P ++WLK NG +
 Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK----NGKEFK 198

Query: 211 PDNLPHYVQILKHSINGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT---- 266
 PD+ ++++ + + +V + G Y C V N G N + L V
 Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVERS 252

Query: 267 -RPVAKA 272
 RP+ +A

Sbjct: 253 HRPILQA 259

sp_vs P11362-5 Isoform 10 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA
 FGFR1_HUMAN (Human)] align

Score = 1275 bits (3299), Expect = 0.0
 Identities = 629/666 (94%), Positives = 641/666 (96%), Gaps = 6/666 (0%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 129
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 189
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYV 247
 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILK +G+N++D E VL L NV+ +GEY
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKTAGVNTTDEKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMGSGVII 307
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSVI+
 Sbjct: 181 CLAGNSIGLSHSHSAWLTVL----EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSIV 236

Query: 308 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 367
 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM
 Sbjct: 237 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 296

Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML
 Sbjct: 297 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356

Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
 Sbjct: 357 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416

Query: 488 RPPGLECYNPNSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 547
 RPPGLECYNPNSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV
 Sbjct: 417 RPPGLECYNPNSHNPPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 476

Query: 548 MKIADFGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL 607
 MKIADFGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL
 Sbjct: 477 MKIADFGLARDIHHIDYYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIPTL 536

Query: 608 GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDLDR 667
 GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDR
 Sbjct: 537 GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 596

Query: 668 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPTQLAN 727
 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHP QLAN
 Sbjct: 597 IVALTSNQEYLDLS+PLDQYSPSPDTRSSSTCSSGEDSVFSHEPLPEEPCLPRHPAQLAN 656

Query: 728 SGLKRR 733
 GLKRR
 Sbjct: 657 GGLKRR 662

sp_vs P11362-6 Isoform 12 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA
 FGFR1_HUMAN (Human)] align

Score = 1266 bits (3277), Expect = 0.0
 Identities = 627/666 (94%), Positives = 639/666 (95%), Gaps = 8/666 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 129
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 189
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSGINSSDAE--VLTLFNVTEAQSGEYV 247
 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILK +G+N++D E VL L NV+ +GEY
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLFPYVQILKTAGVNTTDEKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMGSGVII 307
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSVI+
 Sbjct: 181 CLAGNSIGLSHSHSAWLTVL----EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSIV 236

Query: 308 YKMKSGTKKSDFHQSMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVVRPSRLSSSGTTPM 367

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      YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV  SADSSASMNSGVLLVRPSRLSSSGTPM
Sbjct: 237 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQV - - SADSSASMNSGVLLVRPSRLSSSGTPM 294

Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
      LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML
Sbjct: 295 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 354

Query: 428 KSDATEKDLSDLISEMEMMMKIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
      KSDATEKDLSDLISEMEMMMKIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYLQAR
Sbjct: 355 KSDATEKDLSDLISEMEMMMKIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 414

Query: 488 RPPGLEYCYNPSHNPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 547
      RPPGLEYCYNPSHNPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV
Sbjct: 415 RPPGLEYCYNPSHNPEEQSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNV 474

Query: 548 MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL 607
      MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL
Sbjct: 475 MKIADFGLARDIHHIDYKKTNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTL 534

Query: 608 GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDL 667
      GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE LDR
Sbjct: 535 GGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDR 594

Query: 668 IVALTSNQEYLDLSIPLDQYSPSPFDTRSSTCSSGSDSVFSHEPLPEEPCLPRHPTQLAN 727
      IVALTSNQEYLDLS+PLDQYSPSPFDTRSSTCSSGSDSVFSHEPLPEEPCLPRHP QLAN
Sbjct: 595 IVALTSNQEYLDLSMPLDQYSPSPFDTRSSTCSSGSDSVFSHEPLPEEPCLPRHPAQLAN 654

Query: 728 SGLKRR 733
      GLKRR
Sbjct: 655 GGLKRR 660

sp_vs P21802-3 Isoform 3 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA
      FGFR2_HUMAN (Human)] align

Score = 1108 bits (2867), Expect = 0.0
Identities = 537/694 (77%), Positives = 606/694 (87%), Gaps = 7/694 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWT+ SPEKMEKLLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DA+SSGDEDDTDGAEDFVSENSNNKR - - - APYWTNTEKMEKRLHAVPAANTVFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRVATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
      PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVLLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPYLEIIYCTGAFLISCMGSLVYIYKMKSGTKKSDPHSQMAVHKLAK 330
      +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TTK DF SQ AVHKL K
Sbjct: 362 QAPGREKBITASPDYLEIAIYICIGVFLIACMVVTVILCRMKN+TKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPDRK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYCYNPSHNPEEQSS 508
      IGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGLARDI++IDYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGLARDINNIDYKKT 661

Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVPEELFKLLKEGH 628
      TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYS 781

Query: 689 PSFPDTRSSTCSSGSDSVFSHEPLPEEPCLPRHP 722
      PS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 782 PSYPDTRSS-CSSGDSVFSPPMPYEPCLPQYP 814

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sp_vs P21802-18 Isoform 18 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 820 AA
FGFR2_HUMAN (Human)] align

Score = 1100 bits (2845), Expect = 0.0
Identities = 535/694 (77%), Positives = 604/694 (87%), Gaps = 9/694 (1%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCV VENEYGSINH 242

Query: 151 TYQLDVVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDDVVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINS SDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTREPVA 270
PD LPY+++LKHSGINS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLT V P
Sbjct: 303 PDGLPYLKV LKHSGINS SNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCM LGSVIIYKMKSGTKKSD FHSQMAVHKLAK 330
+A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTIVLCRMKNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQV--SAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 479

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 480 LTLGKPLGEGCFGQVVM AEAGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 539

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPFEQLSS 508
IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 540 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 599

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYKKT 568
KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT
Sbjct: 600 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTE NVMKIADFGGLARDINNIDYKKT 659

Query: 569 TNGRLPVKWM APEALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELPKLLKEGH 628
TNGRLPVKWM APEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELPKLLKEGH
Sbjct: 660 TNGRLPVKWM APEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELPKLLKEGH 719

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYS
Sbjct: 720 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYS 779

Query: 689 PSFPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHP 722
PS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 780 PSYPDTRSS-CSSGDSVFS PDMPYEPCLPQYP 812

sp P21802 Fibroblast growth factor receptor 2 precursor (EC 2.7.10.1) 821 AA
FGFR2_HUMAN (FGFR-2) (Keratinocyte growth factor receptor 2) (CD332 align
antigen) [FGFR2] [Homo sapiens (Human)]

Score = 1065 bits (2755), Expect = 0.0
Identities = 519/696 (74%), Positives = 592/696 (85%), Gaps = 12/696 (1%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCV VENEYGSINH 242

Query: 151 TYQLDVVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDDVVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINS SDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTREP 268
PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLT V
Sbjct: 303 PDGLPYLKV LKAAAGVNTTDKEIEVLVIRNVT FEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPPLYLEIIYCTGAFLISCM LGSVIIYKMKSGTKKSD FHSQMAVHKL 328

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      + E      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 478

Query: 387 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      D+L LGKPLGEGCGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMP
Sbjct: 479 DKLTLGKPLGEGCGQVVMFAVAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 538

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 539 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEENVMKIADFLGLARDIHHIDYYK 566
      + KDLVSC YQ+ARGMEYLA+KCIHRDLAARNVLVTE+NMVKIADFLGLARDI++IDYYK
Sbjct: 599 TFKDLVSCYQLARGMEYLAQKCIHRDLAARNVLVTEENVMKIADFLGLARDINNIDYYK 658

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGSGSPYPGPVEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGSGSPYPG+PVEELFKLLKE
Sbjct: 659 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGSGSPYPGIPVEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
      GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
Sbjct: 719 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQ 778

Query: 687 YSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHP 722
      YSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 779 YSPSYPDTRSS-CSSGDSVFSPPDMPYEPCLPQYP 813

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sp_vs F21802-5      Isoform 5 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA
      FGFR2_HUMAN   (Human)] align

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Score = 1057 bits (2733), Expect = 0.0
Identities = 517/696 (74%), Positives = 590/696 (84%), Gaps = 14/696 (2%)

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Query: 31 DALPSSDDDDDDSSSEKETDNTKPNVPAPYWTSPKMEKKLHAVPAAKTVKFCPS 90
      DA+ S +D+DD D+ E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDTDGAEDFVSESNKNR---APYWTNTEKMEKKLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRVATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNMPTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSHPHPIQLAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSHPHPIQLAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSHPHPIQLAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKEIEVLVIRNVT FEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAVMTSPLYLEIIYCTGAFILSCMLGSVIIYKMKSGTKKSDFHSQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      D+L LGKPLGEGCGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMP
Sbjct: 477 DKLTLGKPLGEGCGQVVMFAVAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEENVMKIADFLGLARDIHHIDYYK 566
      + KDLVSC YQ+ARGMEYLA+KCIHRDLAARNVLVTE+NMVKIADFLGLARDI++IDYYK
Sbjct: 597 TFKDLVSCYQLARGMEYLAQKCIHRDLAARNVLVTEENVMKIADFLGLARDINNIDYYK 656

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGSGSPYPGPVEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGSGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGSGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
      GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+Q
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQ 776

Query: 687 YSPSPDTRSSSTCSSGDSVFSHEPLPEEPCLPRHP 722
      YSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 777 YSPSYPDTRSS-CSSGDSVFSPPDMPYEPCLPQYP 811

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sp_vs P21802-16 Isoform 16 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 822 AA
FGFR2_HUMAN (Human)] align

Score = 1051 bits (2719), Expect = 0.0
Identities = 517/699 (73%), Positives = 590/699 (84%), Gaps = 17/699 (2%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDTDGAEDFVSENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVG DVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILK---HSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTV 265
PD LPY++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLVKLVKLAAGVNTTDKEIEVLYIRNVT FEDAGEYTC LAGNSIGISFHSAWLTV 362

Query: 266 TRPVAKALEERPAVMTSPYLEIIYCTGAPLISCMGSLVYIYKMKSGTKKSDPHSQMAV 325
+ E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AV
Sbjct: 363 LPAPGREKE---ITASPDYLEIAIYCI GVLFIACMVVTIVLCRMKNTTKKPDFSSQPAV 418

Query: 326 HKLAKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWE 383
HKL K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE
Sbjct: 419 HKLTKRIPLRRQV--SAESSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWE 476

Query: 384 LPRDLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEM 443
PRD+L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEM
Sbjct: 477 FPRDKITLGKPLGEGCFGQVVM AEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEM 536

Query: 444 EMMKMIGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPE 503
EMMKMIGKHKNIINLL ACTQDGLYVIVEYASKGNLREYL+ARRPFG+EY Y+ + PE
Sbjct: 537 EMMKMIGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPE 596

Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDEVNMKIADFLGARDIHHD 563
EQ++ KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFLGARDI++ID
Sbjct: 597 EQMTFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTEDEVNMKIADFLGARDIINID 656

Query: 564 YYKKTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGGSYPYGPVPEELFKL 623
YYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSYPYGP+PVEELFKL
Sbjct: 657 YYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSYPYGPVPEELFKL 716

Query: 624 LKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIP 683
LKEGHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS P
Sbjct: 717 LKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQP 776

Query: 684 LDQYSPSPFDRSSTCSSGDSVFSHEPLPEEPCLPRHP 722
L+QYSPS+PDTRSS CSSG+DSVFS +P+P EPCLP++P
Sbjct: 777 LEQYSPSPDTRSS-CSSGDDSVFSPDPMPYEPCLPQYP 814

sp_vs P21802-20 Isoform 20 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 704 AA
FGFR2_HUMAN (Human)] align

Score = 1046 bits (2706), Expect = 0.0
Identities = 520/726 (71%), Positives = 593/726 (81%), Gaps = 34/726 (4%)

Query: 1 MWGKCLLWAVLVATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60
M W + V+ ATL ARP+ +L E D T
Sbjct: 1 MVSWGRFICLVVVTMATLSLARPFSFLVE-----DTTLEPEG 37

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSSGTFNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNGKEFK +HRIGGYKVR
Sbjct: 38 APYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTRWLKNGKEFKQEHRIIGGYKVRNQ 97

Query: 121 TWSIIMDSVVP SDKGNYTCIVENEYGSINH TYQLDVVERSPhRPILQAGLPANKTVALGS 180
WS+IM+SVVP SDKGNYTC+VENEYGSINH TY LDVVERSPhRPILQAGLPAN + +G
Sbjct: 98 HWSLIMESVVP SDKGNYTCVENEYGSINH TYHLDVVERSPhRPILQAGLPANASTVVG 157

Query: 181 NVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTLF--NV 238
+VEF+CKVYSD QPHIQW+KH+E NGSK GPD LPY++LK +G+N++D E+ L+ NV
Sbjct: 158 DVEFVCKVYSDAQPHIQWIKHVEKNGSKYGP DGLPYLVKLAAGVNTTDKEIEVLYIRNV 217

Query: 239 TEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAVMTSPYLEIIYCTGAFLI 298
T +GEY C N IG + SAWLTV + E + SP YLEI IYC G FLI

Sbjct: 218 TFDAGEYTCLAGNSIGISFHSAWLTVLPAPGREKE---ITASPDYLEIAIYCIGVFLI 273

Query: 299 SCMLGSVYIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR-P 357
+CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPLRRQV SA+SS+SMNS LVR

Sbjct: 274 ACMVVTVILCRMKNNTTKPDFSSQPAVHKLTKRIPLRQV--SAESSSSMNSNTPLVRIT 331

Query: 358 SRLSSSG-TPMLAGVSEYELPEDPRWELPRDRVLGKPLGEGCFGQVVLAAEAIGLDKDKP 416
+RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGEGCFGQVVAEA+G+DKDKP

Sbjct: 332 TRLSSTADTPMLAGVSEYELPEDPKWEFFPRDKLTGKPLGEGCFGQVMAEAVGIDKDKP 391

Query: 417 NRVTKVAVKMLKSDATEKDLSLISEMEMMMKIGKHKNIINLLEACTQDGPLYVIVEYAS 476
VAVKMLK DATEKDLSL+SEMEMMMKIGKHKNIINLL ACTQDGPLYVIVEYAS

Sbjct: 392 KEAVTVAVKMLKDDATEKDLSLISEMEMMMKIGKHKNIINLLGACTQDGPLYVIVEYAS 451

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDLVSCAYQVARGMEYLASKKCIHRDLA 536
KGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIHRDLA

Sbjct: 452 KGNLREYLRRARRPPGMEYSYDINRVPEEQMTFKDLVSCYQLARGMEYLASQKCIHRDLA 511

Query: 537 ARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMPEALFDRYTHQSDVWS 596
ARNVLVTE+NVMKIADFGGLARDI++IDYKKTNGRLPVKWMPEALFDR+YTHQSDVWS

Sbjct: 512 ARNVLVTE+NVMKIADFGGLARDIINNIDYKKTNGRLPVKWMPEALFDRVYTHQSDVWS 571

Query: 597 FGVLLWEIFTLGGSFPYGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRP 656
FGVL+WEIFTLGGSFPYGP+PVEELFKLLKEGHRMDKPNCTNELYMMMRDCWHAVPSQRP

Sbjct: 572 FGVLMWEIFTLGGSFPYGPVPEELFKLLKEGHRMDKPNCTNELYMMMRDCWHAVPSQRP 631

Query: 657 TFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDTRSSCTSSGSDSVFSHEPLPEEP 716
TFKQLVE LDRI+ LT+N+EYLDLS PL+QYSPS+PDTRSS CSSG+DSVFS +P+P EP

Sbjct: 632 TFKQLVEDLDRILTLTNEEYLDLSQPLEQYSPSPDTRSS--CSSGSDSVFSPDMPPEP 690

Query: 717 CLPRHP 722
CLP++P

Sbjct: 691 CLPQYP 696

sp_vs P21802-7 Isoform 7 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 817 AA
FGFR2_HUMAN (Human)] align

Score = 1040 bits (2688), Expect = 0.0
Identities = 507/674 (75%), Positives = 571/674 (84%), Gaps = 6/674 (0%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+

Sbjct: 126 DAISSGDEDDDTGAEDFVSSENSNNKR--APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNFTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH

Sbjct: 183 GNPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVEFMCKVSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYS D QPHIQW+KH+E NGSK G

Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVG DVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPHYQILKHSNGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
PD LPY++LKHSGINSS+AEVL LFNVT EA +GEY+CKVSNYIG+ANQSAWLT V P

Sbjct: 303 PDGLPYLKV LKHSNGINSSNAEVLALFNVT EADAGEYICKVSNYIGANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPYLEIIYCTGAFLISCMGLSVIYKMKSGTKKSDPHSQMAVHKLAK 330
+A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K

Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVTVILCRMKNNTTKPDFSSQPAVHKLT 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+

Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMMMK 448
L LGKPLGEGCFGQVVAEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMMMK

Sbjct: 482 LTLGKPLGEGCFGQVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSLISEMEMMMK 541

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+AREPPG+EY Y+ + PEEQ++

Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NVMKIADFGGLARDIHHIDYKKT 568
KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKT

Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDIINNIDYKKT 661

Query: 569 TNGRLPVKWMPEALFDRYTHQSDVWSFGVLLWEIFTLGGSFPYGPVPEELFKLLKEGH 628
TNGRLPVKWMPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSFPYGP+PVEELFKLLKEGH

Sbjct: 662 TNGRLPVKWMPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSFPYGPVPEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPFTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYS 688
RMDKPNCTNELYMMMRDCWHAVPSQRPFTFKQLVE LDRI+ LT+N+ Y L P

Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPFTFKQLVEDLDRILTLTNNERYKLLPCFDKHNK 781

Query: 689 PSFPDTRSSSTCSSG 702
 P+ R +G
 Sbjct: 782 RCKPEERGDLEAG 795

sp_vs P21802-9 Isoform 9 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA
 FGFR2_HUMAN (Human)] align

Score = 1036 bits (2680), Expect = 0.0
 Identities = 503/653 (77%), Positives = 566/653 (86%), Gaps = 6/653 (0%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY+++LKHSGINSS+AEVL LFNVT EA +GEY+CKVSNYIG+ANQSAWLT V P
 Sbjct: 303 PDGLPYLKV LKHSGINSSNAEVLALFNVT EADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPLYLEIIIIYCTGAFLISCMGSLV IYKMKSGTKKSDPHSQMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIYGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
 IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
 Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
 L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
 Sbjct: 482 LTLGKPLGEGCFGQVVM AEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
 IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
 Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDYIYKKT 568
 KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMKIADFGGLARDI++IDYIYKKT
 Sbjct: 602 KDLVSCYQV LARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYIYKKT 661

Query: 569 TNGRLPQVWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVFVEELPKLLKEGH 628
 TNGRLPQVWMAPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELPKLLKEGH
 Sbjct: 662 TNGRLPQVWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELPKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLS 681
 RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ L L+
 Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTITNERILTLT 774

sp_vs P21802-10 Isoform 10 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 819 AA
 FGFR2_HUMAN (Human)] align

Score = 1035 bits (2676), Expect = 0.0
 Identities = 501/649 (77%), Positives = 564/649 (86%), Gaps = 6/649 (0%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAVPAAKTVKFKCPSS 90
 DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
 Sbjct: 126 DAISGGDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
 G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
 Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
 Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
 PD LPY+++LKHSGINSS+AEVL LFNVT EA +GEY+CKVSNYIG+ANQSAWLT V P
 Sbjct: 303 PDGLPYLKV LKHSGINSSNAEVLALFNVT EADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPLYLEIIIIYCTGAFLISCMGSLV IYKMKSGTKKSDPHSQMAVHKLAK 330
 +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
 Sbjct: 362 QAPGREKEITASPDYLEIAIYCIYGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTK 421

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Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
      IGKHKNINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661

Query: 569 TNGRLPVKWMMAPEALFDRITYHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
      TNGRLPVKWMMAPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEQY 677
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+ +
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNESF 770

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sp_vs P21802-11 Isoform 11 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 830 AA
      FGFR2_HUMAN (Human)] align

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Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31 DALPSSDDDDDDSSSEKE'EDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRVATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH
Sbjct: 183 GNMPTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSPDKGNYTCIVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEP+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
      PD LPY+++LKHSGINSS+AEVL LFNVTES +GEY+CKVSNYIG+ANQSAWLT V P
Sbjct: 303 PDGLPYLVKLVKHSGINSSNAEVLALFNVTESADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMLGSVIIYKMSGTTKSDFHQSMAVHKLAK 330
      +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYICGVFLIACMVVTVLICRMKNTTKKPDFSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
      IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
      L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSS 508
      IGKHKNINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNVMKIADFGGLARDIHHIDYYKKT 568
      KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYYKKT 661

Query: 569 TNGRLPVKWMMAPEALFDRITYHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
      TNGRLPVKWMMAPEALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
      RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNE 768

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sp_vs P21802-12 Isoform 12 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 771 AA
      FGFR2_HUMAN (Human)] align

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Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D +      E N K   APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDDTDGAEDFVSENSNNKR-- -APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
          G P PT+RWLKNKGEFK +HRIGGYKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN +   +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMGSGVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTKKPDPSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLKDCKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGLPYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSS 508
          IGKHKNIINLL ACTQDGLPYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIINLLGACTQDGLPYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601

Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI+IDYKKT
Sbjct: 602 KDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661

Query: 569 TNGRLPVKWMAPALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGH 628
          TNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721

Query: 629 RMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNE 768

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sp_vs P21802-13 Isoform 13 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 768 AA
 FGFR2_HUMAN (Human)] align

Score = 1034 bits (2673), Expect = 0.0
 Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31  DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D +      E N K   APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDDTDGAEDFVSENSNNKR-- -APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
          G P PT+RWLKNKGEFK +HRIGGYKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSPDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN +   +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKVLKHSGINSSNAEVLALFNVTEADAGEYICKVSNYIGQANQSAWLTVL-PKQ 361

Query: 271 KALEERPAVMTSPPLYLEIIYCTGAFLISCMGSGVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A      + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTKKPDPSSQPAVHKLTK 421

Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAESSSSMNSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPRDK 481

Query: 389 LVLGKPLGEGCFGQVVLAEAGLKDCKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMABAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541

Query: 449 IGKHKNIINLLEACTQDGLPYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQSS 508
          IGKHKNIINLL ACTQDGLPYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++

```

```

Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601
Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NMVKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYKKT
Sbjct: 602 KDLVSCYQQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661
Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
Query: 629 RMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHA VPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHA VPSQRPTFKQLVEDLDRILTLTTNE 768

```

sp_vs P21802-17 Isoform 17 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 769 AA
FGFR2_HUMAN (Human)] align

Score = 1034 bits (2673), Expect = 0.0
Identities = 501/647 (77%), Positives = 563/647 (87%), Gaps = 6/647 (0%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDEDDDTGAEDFVSESNKKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182
Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNITCIVENEYGSINH 150
          G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVP SDKGNITC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWLIMESVVP SDKGNITCVVENEYGSINH 242
Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSVBFMCKVSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302
Query: 211 PDNLPHYQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVA 270
          PD LPY+++LKHSGINSS+AEVL LFNVTEA +GEY+CKVSNYIG+ANQSAWLTV P
Sbjct: 303 PDGLPYLKLKHSNGINSSNAEVLALFNVTEDAGEYICKVSNYIGQANQSAWLTVL-PKQ 361
Query: 271 KALEERPAVMTSPLYLEIIYCTGAFLISCMLGSVIIYKMKSGTKKSDPHSQMAVHKLAK 330
          +A + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 362 QAPGREKEITASPDYLEIAIYICIGVFLIACMVVTILCRMKNITKKPDFSSQPAVHKLTK 421
Query: 331 SIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDR 388
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+
Sbjct: 422 RIPLRRQVTVSAAESSSSMSNTPLVRITRLSSTADTPMLAGVSEYELPEDPKWEFPDRK 481
Query: 389 LVLGKPLGEGCFGQVVLAEEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKM 448
          L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKM
Sbjct: 482 LTLGKPLGEGCFGQVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKM 541
Query: 449 IGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPPEQLSS 508
          IGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++
Sbjct: 542 IGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQMTF 601
Query: 509 KDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NMVKIADFGGLARDIHHIDYKKT 568
          KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYKKT
Sbjct: 602 KDLVSCYQQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 661
Query: 569 TNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGH 628
          TNGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGH
Sbjct: 662 TNGRLPVKWMapeALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGH 721
Query: 629 RMDKPSNCTNELYMMMRDCWHA VPSQRPTFKQLVEVLDRIVALTSNQ 675
          RMDKP+NCTNELYMMMRDCWHA VPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 722 RMDKPANCTNELYMMMRDCWHA VPSQRPTFKQLVEDLDRILTLTTNE 768

```

sp_vs P21802-4 Isoform 4 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 682 AA
FGFR2_HUMAN (Human)] align

Score = 1029 bits (2661), Expect = 0.0
Identities = 507/676 (75%), Positives = 570/676 (84%), Gaps = 14/676 (2%)

```

Query: 1 MWGKCLLFVAVLVATLCTARPA-----PTLPEQDALPSSDDDDDDSSSEKETDN 54
          M W + V+ ATL ARP+ TL +DA+ S +D+DD D + E N
Sbjct: 1 MVSWGRFICLVVVTMTLSLARPSFSLVEDTTLEPEDAISSGDEDDDTGAEDFVSESN 60
Query: 55 TKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGG 114
          K APYWT+ EKMEK+LHAVPAA TVKF+CP+ G P PT+RWLKNGKEFK +HRIGG
Sbjct: 61 NKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMTMRWLKNGKEFKQEHRIIGG 117
Query: 115 YKVRYATWSIIMDSVVP SDKGNITCIVENEYGSINHTYQLDVVERSPhRPILQAGLPANK 174

```

```

      YKVR  WS+IM+SVVPSDKGNYTC+VENEYGSINHTY LDVVERSPhRPILQAGLPAN
Sbjct: 118 YKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINHTYHLDVVERSPhRPILQAGLPANA 177

Query: 175 TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPYQILKHSGINSSDAEVL 234
      + +G +VEF+CKVSD QPHIQW+KH+E NGSK GPD LPY+++LKHSGINSS+AEVL
Sbjct: 178 STVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDLPLKVLKHSGINSSNAEVL 237

Query: 235 LFNVTQAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIYCTG 294
      LFNVTQA +GEY+CKVSNYIG+ANQSAWLTV P +A + SP YLEI IYC G
Sbjct: 238 LFNVTQADAGEYICKVSNYIGQANQSAWLTVL- PKQQAPGREKETASPDYLEIAIYCTG 296

Query: 295 AFLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLL 354
      FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K IPLRRQV SA+SS+SMNS L
Sbjct: 297 VFLLIACMVVTVILCRMKNNTKKPDPSSQPAVHKLTKRIPLRRQV--SAESSSSMNSNTPL 354

Query: 355 VR-PSRLSSG-TPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFQGVVLAEAIGLD 412
      VR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L LGKPLGEGCFQGVV+AEA+G+D
Sbjct: 355 VRITTRLSTADTPMLAGVSEYELPEDPKWEPFRDKLTGKPLGEGCFQGVVMAEAVGID 414

Query: 413 KDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIV 472
      KDKP VAVKMLK DATEKDLSDL+SEMEMMKMIGKHKNIINLL ACTQDGPLYVIV
Sbjct: 415 KDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMIGKHKNIINLLGACTQDGPLYVIV 474

Query: 473 EYASKGNLREYLQARRPFGLEYCYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIH 532
      EYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ KDLVSC YQ+ARGMEYLAS+KCIH
Sbjct: 475 EYASKGNLREYLARRPFGMEYSYDINRVPEEQMTFKDLVSCYQLARGMEYLASQKCIH 534

Query: 533 RDLAARNVLVTEDNVMKIADFGGLARDIHHIDYKKTNGRLPVKWMAPALFDRYTHQS 592
      RDLAARNVLVTE+NVMKIADFGGLARDI++IDYKKTNGRLPVKWMAPALFDR+YTHQS
Sbjct: 535 RDLAARNVLVTENNVMKIADFGGLARDINNIDYKKTNGRLPVKWMAPALFDRVYTHQS 594

Query: 593 DVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVP 652
      DVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGHRMDK+P+NCTNELYMMMRDCWHAVP
Sbjct: 595 DVWSFGVLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPNCTNELYMMMRDCWHAVP 654

Query: 653 SQRPTFKQLVEVLDRI 668
      SQRPTFKQLVE LDRI
Sbjct: 655 SQRPTFKQLVEDLDRI 670

```

```

tr Q1KHY5 Fibroblast growth factor receptor 2 (Bacteria-expressed kinase, 785 AA
Q1KHY5_HUMAN keratinocyte growth factor receptor, craniofacial
              dysostosis 1, Crouzon syndrome, Pfeiffer syndrome,
              Jackson-Weiss syndrome) [FGFR2] [Homo sapiens (Human)] align

```

Score = 1011 bits (2615), Expect = 0.0
 Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

```

Query: 31 DALPSSSEDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSEDEDDTDGAEDFVSENSNNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNMPTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKLKAAAGVNTTDXEIEVLYIRNVTFEDAGEYTCLAGNSIGISPHSAWLTVLPA 362

Query: 269 VAKALEERPAMVMTSPLYLEIIYCTGAFLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCTGIVFLIACMVVTVILCRMKNNTKKPDPSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWEPFR 476

Query: 387 DRLVLGKPLGEGCFQGVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
      D+L LGKPLGEGCFQGVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 477 DKLTGKPLGEGCFQGVVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPFGLEYCYNPSHNPEEQ 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHHIDYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFGGLARDI++IDYK
Sbjct: 597 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYK 656

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKE 626

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          KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

          GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
Query: 627 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
          GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEP 776
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEP 776

          YSPSPFDTR 695
Query: 687 YSP +PD R
          YSPCYDPDR 785
Sbjct: 777 YSPCYDPDR 785

```

sp_vs P21802-6 Isoform 6 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 785 AA
FGFR2_HUMAN (Human)] align

Score = 1011 bits (2615), Expect = 0.0
Identities = 495/669 (73%), Positives = 563/669 (84%), Gaps = 13/669 (1%)

```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNFVAPYWTSPKMEKKLHAVPAAKTVKFKCPSS 90
          DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISSGDDEDDTDGAEDFVSENSNKR---APYWTNTEKMEKRLHAVPAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
          G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVP SDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPTRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLDVVERSPhRPILQAGLPANKTVALGSGNVFPMCKVYSDPQPHIQWLKHIEVNGSKIG 210
          TY LDVVERSPhRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSPhRPILQAGLPANASTVVGDDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
          PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKBIEVLYIRNVTPEACEYTCLAGNSIGISPHSAWLTVLP 362

Query: 269 VAKALEERPAVMTSPYLEI IYCTGAPLISCMGSLV IYKMKSGTKKSDPHSQMAVHKL 328
          + E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYCIGVFLIACMVVTILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
          K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSMNSNTPLVRITTRLSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCGFQVVLAEAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
          D+L LGKPLGEGCGFQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 477 DKITLGLKPLGEGCGFQVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLRARRPPGLECYCYNPSHNPEEQ 506
          KMIGKHKNIINLL ACTQDGLYVIVEYASKGNLREYLRARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGLYVIVEYASKGNLREYLRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NVMMKIADFGFLARDIHHIDYK 566
          + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMMKIADFGFLARDI++IDYK
Sbjct: 597 TPKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTE+NVMMKIADFGFLARDIINIDYK 656

Query: 567 KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPG+PVEELFKLLKE 626
          KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKE
Sbjct: 657 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQ 686
          GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+
Sbjct: 717 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTTNEEYLDLSQPLEP 776

          YSPSPFDTR 695
Query: 687 YSP +PD R
          YSPCYDPDR 785
Sbjct: 777 YSPCYDPDR 785

```

sp_vs P11362-10 Isoform 7 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 573 AA
FGFR1_HUMAN (Human)] align

Score = 998 bits (2579), Expect = 0.0
Identities = 496/533 (93%), Positives = 508/533 (95%), Gaps = 8/533 (1%)

```

Query: 1 MWGKCLLFWAVLVTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPN-- 58
          MW WKCLLFWAVLVTATLCTARP+PTLPEQDALPSSDDDDDDSSSEKETDNTKPN
Sbjct: 1 MWGKCLLFWAVLVTATLCTARPSPTLPEQDALPSSDDDDDDSSSEKETDNTKPNRM 60

Query: 59 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
          PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61 PVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

```



```

Query: 119 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVAL 178
YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPYVQILKHSGINSSDAE--VLTLF 236
GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANSALWTVTRPVAKALEERPAMVTSPLYLEIIYCTGAF 296
NV+ +GEY C N IG ++ SAWLTV +ALEERPAMVTSPLYLEIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHHSALWTVL---EALERPAVMTSPLYLEIIYCTGAF 296

Query: 297 LISCMGSGVYIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVYIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356

Query: 357 PSRLSSSGTPLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416
PSRLSSSGTPLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP
Sbjct: 357 PSRLSSSGTPLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIAGLDKDKP 416

Query: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYAS 476
NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLL ACTQDGPLYVIVEYAS
Sbjct: 417 NRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYAS 476

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK 529
KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK
Sbjct: 477 KGNLREYLQARRPPGLECYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKK 529

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sp_vs P21802-2      Isoform 2 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 768 AA
FGFR2_HUMAN      (Human)] align

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Score = 991 bits (2561), Expect = 0.0
Identities = 483/649 (74%), Positives = 549/649 (84%), Gaps = 11/649 (1%)

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```

Query: 31 DALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVFAAKTVKFKCPSS 90
DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DAISGDEDDDTGDAEDFVSENSNNKR---APYWTNTEKMEKRLHAVFAANTVKFRCPAG 182

Query: 91 GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINH 150
G P PT+RWLKNKGEFK +HRIGGYKVR WS+IM+SVVPSPDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIGGYKVRNQHWLSIMESVVPSPDKGNYTCVVENEYGSINH 242

Query: 151 TYQLDVVERSHPRPILQAGLPANKTVALGSGNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
TY LDVVERSHPRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLDVVERSHPRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPPYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANSALWTVTRP 268
PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGPLYLKVLAAGVNTTKEIEVLYIRNVTTFEDAGEYTCLAGNSIGISFHSALWTVLPA 362

Query: 269 VAKALEERPAMVTSPLYLEIIYCTGAFLISCMGSGVYIYKMKSGTKKSDFHSQMAVHKL 328
+ E + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE---ITASPDYLEIAIYICGVFLIACMVVTILCRMKNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPLAGVSEYELPEDPRWELPR 386
K IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQVTVSAESSSSSMNSNTPLVRIITRLSSTADTPLAGVSEYELPEDPKWEFPR 478

Query: 387 DRLVLGKPLGEGCFGQVVLAEIAGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
D+L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMM
Sbjct: 479 DKLTDLGKPLGEGCFGQVVMMAEAVGIDKDKPKEAVTVAVKMLKDATEKDLSDLVSEMEMM 538

Query: 447 KMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
KMIGKHKNIIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 539 KMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQM 598

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE+NVMKIADFLGARDIHHIDYK 566
+ KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NVMKIADFLGARDI++IDYK
Sbjct: 599 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFLGARDINNIDYK 658

Query: 567 KTTNGRLPVKWMAPALFDRYTHQSDVWSFGVLLWEIFTLGSGSPYPGVFVEELFKLLKE 626
KTTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGSGSPYG+PVEELFKLLKE
Sbjct: 659 KTTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGSGSPYPGIPVEELFKLLKE 718

Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQ 675
GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+
Sbjct: 719 GHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNE 767

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sp_vs P11362-11     Isoform 9 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 571 AA
FGFR1_HUMAN      (Human)] align

```

Score = 989 bits (2557), Expect = 0.0
Identities = 494/533 (92%), Positives = 506/533 (94%), Gaps = 10/533 (1%)

```

Query: 1  MWGKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN-- 58
      MW WKCLLFWAVLVLTATLCTARP+PTLPEQDALPSSSEDDDDDDSSSEKETDNTKPN
Sbjct: 1  MWSKCLLFWAVLVLTATLCTARPSPTLPEQDALPSSSEDDDDDDSSSEKETDNTKPNRM 60

Query: 59  PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 118
      PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR
Sbjct: 61  PVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSSGTPNPTLRWLKNGKEFKPDHRIGGYKVR 120

Query: 119 YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL 178
      YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL
Sbjct: 121 YATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLD VVERS PHRPILQAGLPANKTVAL 180

Query: 179 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKHSGINSSDAE--VLTLF 236
      GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILK +G+N++D E VL L
Sbjct: 181 GSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPHYVQILKTAGVNTTDKEMEVLHLR 240

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIIIYCTGAF 296
      NV+ +GEY C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAF
Sbjct: 241 NVSFEDAGEYTCLAGNSIGLSHSAWLTVL---EALERPAVMTSPLYLEIIIIYCTGAF 296

Query: 297 LISCM LGSVIIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVR 356
      LISCM+GSVI+YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVR
Sbjct: 297 LISCMVGSVIVYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVR 354

Query: 357 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEI GLDKDKP 416
      PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEI GLDKDKP
Sbjct: 355 PSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEI GLDKDKP 414

Query: 417 NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYAS 476
      NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYAS
Sbjct: 415 NRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYAS 474

Query: 477 KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 529
      KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK
Sbjct: 475 KGNLREYLQARRPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 527

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sp_vs P21802-8 Isoform 8 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 766 AA align
FGFR2_HUMAN (Human)]

Score = 982 bits (2539), Expect = 0.0
Identities = 481/649 (74%), Positives = 547/649 (84%), Gaps = 13/649 (2%)

```

Query: 31  DALPSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSS 90
      DA+ S +D+DD D + E N K APYWT+ EKMEK+LHAVPAA TVKF+CP+
Sbjct: 126 DATSSGDEDDDDTGAEDFVSENSNKR---APYWTNTEKMEKRLHAVPAANTVVFRCFAG 182

Query: 91  GTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINH 150
      G P PT+RWLKNNGKEFK +HRIGGYKVR WS+IM+SVVPSDKGNYTC+VENEYGSINH
Sbjct: 183 GNPMPMTMRWLKNGKEFKQEHRIIGGYKVRNQHWSLIMESVVP SDKGNYTCVENEYGSINH 242

Query: 151 TYQLD VVERS PHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
      TY LDVVERS PHRPILQAGLPAN + +G +VEF+CKVYSD QPHIQW+KH+E NGSK G
Sbjct: 243 TYHLD VVERS PHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYG 302

Query: 211 PDNLPHYVQILKHSGINSSDAEVLTLF--NVTEAQSGEYVCKVSNYIGEANQSAWLTVTRP 268
      PD LPY+++LK +G+N++D E+ L+ NVT +GEY C N IG + SAWLTV
Sbjct: 303 PDGLPYLKVLAAGVNTTDKEIEVLVIRNVT FEDAGEYTCLAGNSIGISFHSAWLTVLPA 362

Query: 269 VAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCM LGSVIIYKMKSGTKKSDFHSQMAVHKL 328
      + E + SP YLEI IYC G FLI+CM++VI+ +MK+ TKK DF SQ AVHKL
Sbjct: 363 PGREKE----ITASPDYLEIAIYCIGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKL 418

Query: 329 AKSIPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPR 386
      K IPLRRQV SA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PR
Sbjct: 419 TKRIPLRRQV--SAESSSMNSNTPLVRITRLSSSTADTPMLAGVSEYELPEDPKWEFPR 476

Query: 387 DRLVLGKPLGEGCFGQVVLAEI GLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMM 446
      D+L LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSL+SEMEMM
Sbjct: 477 DKLT LGKPLGEGCFGQVVM AEAVGIDKDKPEAVTVAVKMLKD DATEKDLSLSEMEMM 536

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ L 506
      KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ+
Sbjct: 537 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLRRARRPPGMEYSYDINRVPEEQM 596

Query: 507 SSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTE DNVMKIAD FGLARDIHHIDYYK 566
      + KDLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+DNVMKIAD FGLARDI++IDYYK
Sbjct: 597 TFKDLVSCYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIAD FGLARDINNIDYYK 656

Query: 567 KTTNGRLPVKWMAPALFDRIYTHQSDVVSFGVLLWEIFTLGGSYPYGPVPEELFKLLKE 626
      KTTNGRLPVKWMAPALFDR+YTHQSDVVSFGVL+WEIFTLGGSYPYGP+PVEELFKLLKE

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Sbjct: 657 KTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKE 716
 Query: 627 GHRMDKPSNCTNELYMMMRDCWHAVPSQRPTPKQLVEVLDRIVALTSNQ 675
 GHRMDKP+NCTNELYMMMRDCWHAVPSQRPTPKQLVE LDRI+ LT+N+
 Sbjct: 717 GHRMDKPFANCTNELYMMMRDCWHAVPSQRPTPKQLVEDLDRIILTITNE 765

sp_vs P11362-8 Isoform 2 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 662 AA
 FGFR1_HUMAN (Human)] align

Score = 934 bits (2415), Expect = 0.0
 Identities = 468/503 (93%), Positives = 479/503 (95%), Gaps = 8/503 (1%)

Query: 31 DALPSSDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179
 Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDCKGNYTCIVENEYGS 148
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDCKGNYTCIVENEYGS
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDCKGNYTCIVENEYGS 239
 Query: 149 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVVERSHPRPILQAGLPANKTVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299
 Query: 209 IGPDLNLPYVQILKHSGINSSDAE--VLTLEFNVTQAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL 359
 Query: 267 RPAKALEERPAVMTSPLYLEIIIIYCTGAFLISCMVGSIIYKMKSGTKKSDPHSQMAVH 326
 +ALEERPAVMTSPLYLEIIIIYCTGAFLISCM+GSVI+YKMKSGTKKSDPHSQMAVH
 Sbjct: 360 ----EALERPAVMTSPLYLEIIIIYCTGAFLISCMVGSIVIVYKMKSGTKKSDPHSQMAVH 415
 Query: 327 KLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 386
 KLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR
 Sbjct: 416 KLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPR 475
 Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM
 Sbjct: 476 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 535
 Query: 447 KMIGKHKNIINLLACTQDGPPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
 KMIGKHKNIINLL ACTQDGPPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ
 Sbjct: 536 KMIGKHKNIINLLGACTQDGPPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 595
 Query: 507 SSKDLVSCAYQVARGMEYLASKK 529
 SSKDLVSCAYQVARGMEYLASKK
 Sbjct: 596 SSKDLVSCAYQVARGMEYLASKK 618

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVLTATLCTARPAPTLPEQDALPSSDDDDDDSSSEKETDNTKPNPV 60
 MW WKCLLFWAVLVLTATLCTARP+PTLPEQ
 Sbjct: 1 MWSWKCLLFWAVLVLTATLCTARPSPTLPEQ----- 30
 Query: 61 APYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R
 Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLRCLRLDDVQ--SINWLRDGVQLAESNR-----TRIT 82
 Query: 121 TWSIIMDSVVPDCKGNYTCIVENEYGSINHTYQLDVVERS----- 161
 + + VP+D G Y C+ + GS + ++V + P
 Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSSDDDDDDSSSEKETD 142
 Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 P+ K V V+P C P P ++WLK NG +
 Sbjct: 143 NTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK----NGKEFK 198
 Query: 211 PDNLPYVQILKHSGINSSDAEVLTLFNVTQAQSGEYVCKVSNYIGEANQSAWLTVT---- 266
 PD+ ++++ + + +V + G Y C V N G N + L V
 Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVPDCKGNYTCIVENEYGSINHTYQLDVVERS 252
 Query: 267 -RPVAKA 272
 RP+ +A
 Sbjct: 253 HRPILQA 259

sp P22607 Fibroblast growth factor receptor 3 precursor (EC 2.7.10.1) 806 AA
 FGFR3_HUMAN (FGFR-3) (CD333 antigen) [FGFR3] [Homo sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAPPAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
 Sbjct: 129 PSSGDDDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVENKFGSIRQTYT 242

Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSHPRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
 Sbjct: 243 LDVLERSPHRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDPG 302

Query: 214 LPYVQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPAK 271
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
 Sbjct: 303 TPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSSHSAWLVVL-PAEE 361

Query: 272 ALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIIYKMKSGTKKSDFHQSMAVHKLAKS 331
 L E A +Y I+ Y G FL ++ +V + +++S KK VHK+++
 Sbjct: 362 ELVE--ADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKKG--LGSPTVHKISR- 416

Query: 332 IPLRRQVTVSADSSASMSNGVLLVVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L
 Sbjct: 417 FPLKRQV--SLESNASMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 474

Query: 392 GKPLGEGCFGQVVLAAEIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451
 GKPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGK
 Sbjct: 475 GKPLGEGCFGQVMAEAIGIDKRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGK 534

Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPPEQLSSKDL 511
 HKNIINLL ACTQ GPLYV+VEYA-KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL
 Sbjct: 535 HKNIINLLGACTQGGPLYVVLVEYAAKGNLREPLRARRPPGLDYSEDTCKPPEQLTFKDL 594

Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMKIADFGGLARDIHHIDYKKTNG 571
 VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEEDNMKIADFGGLARD+H++DYKKTNG
 Sbjct: 595 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEEDNMKIADFGGLARDVHNLDDYKKTNG 654

Query: 572 RLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMD 631
 RLPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMD
 Sbjct: 655 RLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMD 714

Query: 632 KPSNCTNELYMMMRDCWHAHVPSQRPTFFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSF 691
 KP+NCT++LYM+MR+CWAH PSQRPTFFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 715 KPANCTHDLYMIMRECWAHAPSQRPTFFKQLVEDLDRVLTSTDEYLDLSAPFQYSPSG 774

Query: 692 PDTRSSTCSSGDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 775 QDTPSSS-SSGDSVFAHDLPPAP 798

tr Q8NI15 Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo 769 AA
 Q8NI15_HUMAN sapiens (Human)] align

Score = 931 bits (2406), Expect = 0.0
 Identities = 462/685 (67%), Positives = 552/685 (80%), Gaps = 17/685 (2%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPPEKMEKKLHAPPAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
 Sbjct: 92 PSSGDDDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 145

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 146 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVENKFGSIRQTYT 205

Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSHPRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
 Sbjct: 206 LDVLERSPHRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDPG 265

Query: 214 LPYVQILKHSGINSDDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPAK 271
 PYV +LK +G N++D E VL+L NVT +GEY C N IG ++ SAWL V P +
 Sbjct: 266 TPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSSHSAWLVVL-PAEE 324

Query: 272 ALEERPAVMTSPLYLEIIYCTGAFLISCMGLSVIIYKMKSGTKKSDFHQSMAVHKLAKS 331
 L E A +Y I+ Y G FL ++ +V + +++S KK VHK+++
 Sbjct: 325 ELVE--ADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKKG--LGSPTVHKISR- 379

Query: 332 IPLRRQVTVSADSSASMSNGVLLVVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL L
 Sbjct: 380 FPLKRQV--SLESNASMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 437

Query: 392 GKPLGEGCFGQVVLAAEIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451
 GKPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGK

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Sbjct: 438 GKPLGEGCGFQVVMMAEAGIDKDRRAKPVTVAVKMLKDDATDKDLSDLVSEMMEKMGK 497
Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDL 511
      HKNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDL
Sbjct: 498 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQQLTFKDL 557
Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMKIADFGGLARDIHHIDYKKTNG 571
      VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEEDNMKIADFGGLARD+H++DYKKTNG
Sbjct: 558 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEEDNMKIADFGGLARDVHNLDYKKTNG 617
Query: 572 RLPVKWMAPEALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMD 631
      RLPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMD
Sbjct: 618 RLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMD 677
Query: 632 KPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPF 691
      KP+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
Sbjct: 678 KPANCHDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGG 737
Query: 692 PDTRSSCTSSGSDSVFSHEPLPEEP 716
      DT SS+ SSG+DSVF+H+ LP P
Sbjct: 738 QDTPSSS-SSGDDSVFAHDLPPAP 761

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tr Q8NI16      Fibroblast growth factor receptor 3 (Fragment) [FGFR3] [Homo 771 AA
Q8NI16_HUMAN sapiens (Human)] align

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Score = 929 bits (2402), Expect = 0.0
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)

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Query: 34  PSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTP 93
      PSS DD+D +D      E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
Sbjct: 92  PSSGDDDEDGED-----EADTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 145
Query: 94  NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQ 153
      P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
Sbjct: 146 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVP SDRGNYTCVENKFGSIRQTYT 205
Query: 154 LDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPOPHIQWLKHIEVNGSKIGPDN 213
      LDV+ERSPHRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
Sbjct: 206 LDVLESPHRPILQAGLPANQTAVLGSDFEFCKVYSDAQPHIQWLKHVEVNGSKVGPDPG 265
Query: 214 LPYVQILKHSINGSSDAEV-LTLEFNVTQAQSGEYVCKVSNYIGEANQSAWLTVPVAKA 272
      PYV +LK      S +A+V L L NV+E GEY+C+ +N+IG A ++ WL+V P A
Sbjct: 266 TPYVTVLKSWISEVADVRLRLANVSRDGGEYLCRATNFIGVAEKAFWLSVHGPPRAAE 325
Query: 273 LEERPAVMTSPLYLEIIIIYCTGAFLISCMLGSVIIYKMKSGTKKSDFHSMQMAVHKLAKSI 332
      E A      +Y I+ Y G FL ++ +V + +++S KK      VHK+++
Sbjct: 326 EELVEADEAGSSVYAGILSYGVGFLLFILVVAATLCLRLSPPKKG--LGSPTVHKISR-F 382
Query: 333 PLRRQVTVSADSSASMNSGVLVLRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDLVLVG 392
      PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL LG
Sbjct: 383 PLKRQV--SLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTG 440
Query: 393 KPLGEGCGFQGVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKH 452
      KPLGEGCGFQGVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMMEKMGKH
Sbjct: 441 KPLGEGCGFQVVMMAEAGIDKDRRAKPVTVAVKMLKDDATDKDLSDLVSEMMEKMGKH 500
Query: 453 KNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQQLSSKDLV 512
      KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV
Sbjct: 501 KNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQQLTFKDLV 560
Query: 513 SCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMKIADFGGLARDIHHIDYKKTNGR 572
      SCAYQVARGMEYLAS+KCIHRDLAARNVLVTEEDNMKIADFGGLARD+H++DYKKTNGR
Sbjct: 561 SCAYQVARGMEYLASQKCIHRDLAARNVLVTEEDNMKIADFGGLARDVHNLDYKKTNGR 620
Query: 573 LPVKWMAPEALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDK 632
      LPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMDK
Sbjct: 621 LPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDK 680
Query: 633 PSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPFP 692
      P+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
Sbjct: 681 PANCHDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQ 740
Query: 693 DTRSSCTSSGSDSVFSHEPLPEEP 716
      DT SS+ SSG+DSVF+H+ LP P
Sbjct: 741 DTPSSS-SSGDDSVFAHDLPPAP 763

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sp_vs F22607-2      Isoform 2 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens 808 AA
FGFR3_HUMAN (Human)] align

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Score = 929 bits (2402), Expect = 0.0
 Identities = 459/684 (67%), Positives = 551/684 (80%), Gaps = 13/684 (1%)

Query: 34 PSSSEDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPA TV+F+CP++G P
 Sbjct: 129 PSSGDEDEDGED-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 183 TPISISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVENKFGSIRQTYT 242

Query: 154 LDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSPhRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
 Sbjct: 243 LDVLERSPhRPILQAGLPANQTAVLGSDFEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 302

Query: 214 LPYVQILKHSNGINSSDAEV-LTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVPVAKA 272
 PYV +LK S +A+V L L NV+E GEY+C+ +N+IG A ++ WL+V P A
 Sbjct: 303 TPYVTVLKSWISESVEADVRLRLANVSERDGGEYLCRATNFIGVAEKAFLSVHGPRAAE 362

Query: 273 LEERPAVMTSPPLYLEIIYCTGAFLISCMGSLVIIYKMKSGTKKSDFHSQMAVHKLAKSI 332
 E A +Y I+ Y G FL ++ +V + ++S KK VHK+++
 Sbjct: 363 EELVEADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLSPPKKG--LGSPTVHKISR-F 419

Query: 333 PLRRQVTVSADSSASMNsgvllvrpsrlsssgtpmlagvseyelpedprwelprdrvlvg 392
 PL+RQV S +S+ASM+S LVR +RLSS P LA VSE ELP DP+WEL R RL LG
 Sbjct: 420 PLKRQV--SLESNASMSsntplvriarllsssgcptlanvselelpadpkwelsrarltlg 477

Query: 393 KPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKH 452
 KPLGEGCFGQVV+AEAIG+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGKH
 Sbjct: 478 KPLGEGCFGQVVMAEAIGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGKH 537

Query: 453 KNIINLLEACTQDGLYVIVEYASKNLRREYLQARRPPGLECYCNPSPHNPEEQLSKDLV 512
 KNIINLL ACTQ GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLV
 Sbjct: 538 KNIINLLGACTQGGLYVLYVEYAAKGNLREPLRARPPGLDYSFDTCKPPPEQLTFKDLV 597

Query: 513 SCAYQVARGMEYLASKKCIHRDLAARNVLVTEEDNMKIADFGGLARDIHIDYVKKTTNGR 572
 SCAYQVARGMEYLAS+KCIHRDLAARNVLVTEEDNMKIADFGGLARD+H++DYVKKTTNGR
 Sbjct: 598 SCAYQVARGMEYLASQKCIHRDLAARNVLVTEEDNMKIADFGGLARDVHNLDYVKKTTNGR 657

Query: 573 LPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGPVEELFKLLKEGHRMDK 632
 LPVKWMAPEALFDR+YTHQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMDK
 Sbjct: 658 LPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGPVVEELFKLLKEGHRMDK 717

Query: 633 PSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPFP 692
 P+NCT++LYM+MR+CWHA PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP
 Sbjct: 718 PANCTHDLYMIMRECWAAPSQRPPTFKQLVEDLDRVLTVTSTDEYLDLSAPPEQYSPGGQ 777

Query: 693 DTRSTCSCSGEDSVFSHEPLPEEP 716
 DT SS+ SSG+DSVF+H+ LP P
 Sbjct: 778 DTPSSS-SSGDSVFAHDLPLPPAP 800

sp_vs P11362-9 Isoform 5 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 660 AA
 FGFR1_HUMAN (Human)] align

Score = 926 bits (2393), Expect = 0.0
 Identities = 466/503 (92%), Positives = 477/503 (94%), Gaps = 10/503 (1%)

Query: 31 DALPSSSEDDDDDDSSSEKETDNTKPN--PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 88
 DALPSSSEDDDDDDSSSEKETDNTKPN PVAPYWTSPEKMEKKLHAVPAAKTVKFKCP
 Sbjct: 120 DALPSSSEDDDDDDSSSEKETDNTKPNRMPVAPYWTSPEKMEKKLHAVPAAKTVKFKCP 179

Query: 89 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI 148
 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI
 Sbjct: 180 SSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSI 239

Query: 149 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 208
 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK
 Sbjct: 240 NHTYQLDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSK 299

Query: 209 IGPDLNLPYVQILKHSNGINSSDAE--VLTFLNVTEAQSGEYVCKVSNYIGEANQSAWLTVT 266
 IGPDLNLPYVQILK +G+N++D E VL L NV+ +GEY C N IG ++ SAWLTV
 Sbjct: 300 IGPDLNLPYVQILKTAGVNTTDKEMEVLHLRNVSPFDAGEYTCLAGNSIGLSHHSAWLTVL 359

Query: 267 RPAKALEERPAVMTSPPLYLEIIYCTGAFLISCMGSLVIIYKMKSGTKKSDFHSQMAVH 326
 +ALEERPAVMTSPPLYLEIIYCTGAFLISCM+GSVI+YKMKSGTKKSDFHSQMAVH
 Sbjct: 360 ----EALERPAVMTSPPLYLEIIYCTGAFLISCMVGSVIVYKMKSGTKKSDFHSQMAVH 415

Query: 327 KLAksiPLRRQVTVSADSSASMNsgvllvrpsrlsssgtpmlagvseyelpedprwelpr 386
 KLAksiPLRRQV SADSSASMNsgvllvrpsrlsssgtpmlagvseyelpedprwelpr
 Sbjct: 416 KLAksiPLRRQV--SADSSASMNsgvllvrpsrlsssgtpmlagvseyelpedprwelpr 473

Query: 387 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMM 446
 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMM

Sbjct: 474 DRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMM 533

Query: 447 KMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 506
 KMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ

Sbjct: 534 KMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQ 593

Query: 507 SSKDLVSCAYQVARGMEYLASKK 529
 SSKDLVSCAYQVARGMEYLASKK

Sbjct: 594 SSKDLVSCAYQVARGMEYLASKK 616

Score = 90.5 bits (223), Expect = 9e-18
 Identities = 78/307 (25%), Positives = 118/307 (38%), Gaps = 83/307 (27%)

Query: 1 MWGWKCLLFWAVLVTATLCTARPAPTLPEQDALPSEDDDDDDSSSEKETDNTKPNPV 60
 MW WKCLLFWAVLVTATLCTARP+PTLPEQ

Sbjct: 1 MWSWKCLLFWAVLVTATLCTARPSPTLPEQ----- 30

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
 A W +P ++E L V ++ +C ++ WL++G + +R R

Sbjct: 31 AQPWGAPVEVESFL--VHPGDLQLRCRLRDDVQ-SINWLRDGVQLAESNR-----TRIT 82

Query: 121 TWSIIMDSVVP SDKGN YTCIVENEYGSINHTYQLDVVERSP----- 161
 + + VP+D G Y C+ + GS + ++V + P

Sbjct: 83 GEEVEVQDSVPADSGLYACVTSSPSGSDTTYFSVNVSDALPSEDDDDDDSSSEKETD 142

Query: 162 -----HRPILQAGLPANK-----TVALGNSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIG 210
 P+ K V V+F C P P ++WLK NG +

Sbjct: 143 NTKPNRMPVAPYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLK---NGKEFK 198

Query: 211 PDNLPYVQILKHSGINS SDAEVLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVT--- 266
 PD+ +++ + + +V + G Y C V N G N + L V

Sbjct: 199 PDHRIGGYKVRYATWS-----IIMDSVVP SDKGN YTCIVENEYGSINHTYQLDVVERSP 252

Query: 267 -RPVAKA 272
 RP+ +A

Sbjct: 253 HRPILQA 259

sp_vs P11362-12 Isoform 11 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 502 AA
 FGFR1_HUMAN (Human)] align

Score = 857 bits (2214), Expect = 0.0
 Identities = 429/462 (92%), Positives = 440/462 (95%), Gaps = 6/462 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV

Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGN YTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY 189
 VPSDKGN YTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY

Sbjct: 61 VPSDKGN YTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTVALGNSNVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGFDNLPYVQILKHSGINS SDAE--VLTFLFNVTEAQSGEYV 247
 SDPQPHIQWLKHIEVNGSKIGFDNLPYVQILK +G+N++D E VL L NV+ +GEY

Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGFDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVTRPVAKALEERP AVMTSPLYLEIIYCTGAPLISCM LGSV I 307
 C N IG ++ SAWLTV +ALEERP AVMTSPLYLEIIYCTGAPLISCM +GSVI+

Sbjct: 181 CLAGNSIGLSHHS AWLTVL---EALERP AVMTSPLYLEIIYCTGAPLISCMVGSV I 236

Query: 308 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM 367
 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM

Sbjct: 237 YKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPM 296

Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML

Sbjct: 297 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 356

Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMKMIGKHKNIINLL ACTQDGPLYVIVEYASKGNLREYLQAR

Sbjct: 357 KSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQAR 416

Query: 488 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 529
 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK

Sbjct: 417 RPPGLECYNPSHNPEEQ LSSKDLVSCAYQVARGMEYLASKK 458

sp_vs P11362-13 Isoform 13 of P11362 - Homo sapiens (Human) [FGFR1] [Homo sapiens 500 AA
 FGFR1_HUMAN (Human)] align

Score = 848 bits (2192), Expect = 0.0
 Identities = 427/462 (92%), Positives = 438/462 (94%), Gaps = 8/462 (1%)

Query: 70 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 129
 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV
 Sbjct: 1 MEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSV 60

Query: 130 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVY 189
 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVY
 Sbjct: 61 VPSDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVY 120

Query: 190 SDPQPHIQWLKHIEVNGSKIGPDNLPHYQILKHSGINSSDAE--VLTLFNVTEAQSGEYV 247
 SDPQPHIQWLKHIEVNGSKIGPDNLPHYQILK +G+N++D E VL L NV+ +GEY
 Sbjct: 121 SDPQPHIQWLKHIEVNGSKIGPDNLPHYQILKTAGVNTTDKEMEVLHLRNVSPEDAGEYT 180

Query: 248 CKVSNYIGEANQSAWLTVPVAKALEERPAMVMTSPLYLEIIIIYCTGAFLISCMGSGVII 307
 C N IG ++ SAWLTV +ALEERPAMVMTSPLYLEIIIIYCTGAFLISCM+GSGVI+
 Sbjct: 181 CLAGNSIGLSHSAWLTVL---EALERPAMVMTSPLYLEIIIIYCTGAFLISCMVGSVIV 236

Query: 308 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTGM 367
 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV SADSSASMNSGVLLVRPSRLSSSGTGM
 Sbjct: 237 YKMKSGTKKSDFHSQMAVHKLAKSIPLRRQV--SADSSASMNSGVLLVRPSRLSSSGTGM 294

Query: 368 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 427
 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML
 Sbjct: 295 LAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKML 354

Query: 428 KSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQAR 487
 KSDATEKDLSDLISEMEMMKMIGKHKNIIINL ACTQDGPLYVIVEYASKGNLREYLQAR
 Sbjct: 355 KSDATEKDLSDLISEMEMMKMIGKHKNIIINL GACTQDGPLYVIVEYASKGNLREYLQAR 414

Query: 488 RPPGLECYCNPSHNPFEELSSKDLVSCAYQVARGMEYLASKK 529
 RPPGLECYCNPSHNPFEELSSKDLVSCAYQVARGMEYLASKK
 Sbjct: 415 RPPGLECYCNPSHNPFEELSSKDLVSCAYQVARGMEYLASKK 456

sp P22455 Fibroblast growth factor receptor 4 precursor (EC 2.7.10.1) 802 AA
 FGFR4_HUMAN (FGFR-4) (CD334 antigen) [FGFR4] [Homo sapiens (Human)] align

Score = 839 bits (2168), Expect = 0.0
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPKME 71
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME
 Sbjct: 100 LCLARGSMIVLQNLTITGDSLTSS--NDEDFKSHRDPNSNRHSYPQQ-APYWTHPQRM 156

Query: 72 KKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP
 Sbjct: 157 KKLHAVPAGNTVVKFRCPAAGNPTPTIRWLKDGQAAPHGENRIGGIRLRHQHWSLVMSVVP 216

Query: 132 SDKGNITCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGNSVEFMCKVYSD 191
 SD+G YTC+VEN GSI + Y LDV+ERSHPRPILQAGLPAN T +GS+VE +CKVYSD
 Sbjct: 217 SDRGTYTCLVENAVGSIRYNYLLDVLEERSHPRPILQAGLPANTTAVVGSDELCKVYSD 276

Query: 192 PQPHIQWLKHIEVNGSKIGPDNLPHYQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVS 251
 QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C
 Sbjct: 277 AQPHIQWLKHIVINGSSPGADGPPYVQVLKTADINSSEVEVLRLNVSAEDAGEYTCLAG 336

Query: 252 NYIGEANQSAWLTVPVAKALEERP---AVMTSPLYLEIIIIYCTGAFLISCMGSGVII 308
 N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L +Y
 Sbjct: 337 NSIGLSYQSAWLTVLP-----BEDPTWTAAPEARYTDIILYASGSLALAVLLLLAGLY 390

Query: 309 KMKSGTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTP 366
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG
 Sbjct: 391 R---GQALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGPA 444

Query: 367 MLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKM 426
 +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKM
 Sbjct: 445 LLAGLVSLDPLDPLWEFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKM 504

Query: 427 LKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQA 486
 LK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+A
 Sbjct: 505 LKDNASDKDLADLVSEMEVMKLGHRKNIIINLLGVCTQEGPLYVIVECAAKGNLREFLRA 564

Query: 487 RPPGLECYCNPSHNPFEELSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546
 RRPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN
 Sbjct: 565 RRPPGPDLSPDGPRSSGFLSFPVLVSCAYQVARGMYLESRKCIHRDLAARNVLVTEDN 624

Query: 547 VMKIADPGLARDIHHIDYKKTNGRLPVKWMPEALFDRIYTHQSDVWSFGVLLWEIFT 606
 VMKIADPGLAR +HHIDYKKT+NGRLPVKWMPEALFDR+YTHQSDVWSFG+LLWEIFT
 Sbjct: 625 VMKIADPGLARGVHHIDYKKTNGRLPVKWMPEALFDRVYTHQSDVWSFGILLWEIFT 684

Query: 607 LGGSFPYGPVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLD 666
 LGGSFPYGP+PVEELF LL+EGHRMD+P +C ELY +MR+CWA PSQRPTFKQLVE LD

Sbjct: 685 LGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALD 744
 Query: 667 RIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLP 713
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
 Sbjct: 745 KVL-LAVSEEYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 788

tr Q8TDA0 Fibroblast growth factor receptor 4 (Fibroblast growth factor 802 AA
 Q8TDA0_HUMAN receptor 4, isoform CRA_b) [FGFR4] [Homo sapiens align
 (Human)]

Score = 839 bits (2167), Expect = 0.0
 Identities = 432/707 (61%), Positives = 527/707 (74%), Gaps = 29/707 (4%)

Query: 18 LCTARPAP-----TLPEQDALPSSDDDDDDSSSEKETDNTKPNPVAPYWTSPEKME 71
 LC AR + TL D+L SS +DD+D S + ++ P APYWT P++ME
 Sbjct: 100 LCLARGSMIVLQNLTLITGDSLTS--NDEDEPKSHRDLNHRHSYPQQ-APYWTHPQRM 156
 Query: 72 KKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 131
 KKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG ++R+ WS++M+SVVP
 Sbjct: 157 KKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIRLRHQHNSLVMSVVP 216
 Query: 132 SDKGNYTCIVENEYGSINHTYQLDVVERSHPHPILOAGLPANKTVALGNSNVEFMCKVYSD 191
 SD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD
 Sbjct: 217 SDRGTYTCLVENAVGSIRYNLLDVLERSPHRPILQAGLPANTTAVVGSVDVLLCKVYSD 276
 Query: 192 QPHIQWLKHIEVNGSKIGPDNLFPYVQILKHSINGSSDAEVLTLFNVTEAQSGEYVCKVS 251
 QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C
 Sbjct: 277 AQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAG 336
 Query: 252 NYIGEANQSAWLTVTRPVAKALEERP---AVMTSPLEYLEIIYCTGAFLISCMGLGSVIIY 308
 N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L +Y
 Sbjct: 337 NSIGLSYQSAWLTVLP-----EEDPTWTAAPPEARYTDIILYASGSLALAVLLLAGLY 390
 Query: 309 KMKSGTKKSDPHSQ--MAVHKLAKSIPLRRQVTVSADSSASMSGVLLVRPSRLSSSGTP 366
 + G H + V KL++ PL RQ ++ + SS +S LVR RLSSSG
 Sbjct: 391 R---GQALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRLSSSGPA 444
 Query: 367 MLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEIGLDKDKPNRVTKVAVKM 426
 +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKM
 Sbjct: 445 LLAGLVSLDLPLDPLWEFPDRDLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKM 504
 Query: 427 LKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGLYVIVEYASKGNLREYLQA 486
 LK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+A
 Sbjct: 505 LKDNASDKDLADLVSEMEVMKLGIRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRA 564
 Query: 487 RRPPGLECYCYNFSHPNEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDN 546
 RRPPG + + - E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDN
 Sbjct: 565 RRPPGPDLSPDGPRSSGGLSFPVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDN 624
 Query: 547 VMKIADFLGARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLWEIFT 606
 VMKIADFLGAR +HHIDYKKT+NGRLPVKWMAPALFDR+YTHQSDVWSFG+LLWEIFT
 Sbjct: 625 VMKIADFLGARGVHHIDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGILLWEIFT 684
 Query: 607 LGGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSPQRPTFKQLVEVLD 666
 LGGSPYPG+PVEELF LL+EGHRMD+P+C ELY +MR+CWHA PSQRPTFKQLVE LD
 Sbjct: 685 LGGSPYPGIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQLVEALD 744
 Query: 667 RIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGSDSVFSHEPLP 713
 +++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
 Sbjct: 745 KVL-LAVSEEYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 788

tr Q71TW8 Fibroblast growth factor receptor 4, soluble-form splice variant 762 AA
 Q71TW8_HUMAN [FGFR4] [Homo sapiens (Human)] align

Score = 805 bits (2078), Expect = 0.0
 Identities = 414/700 (59%), Positives = 501/700 (71%), Gaps = 55/700 (7%)

Query: 18 LCTARPAPTLPEQDAL---PSSDDDDDDSSSEKETDNTKPNPVAPYWTSPEKMEKK 73
 LC AR + + + L S+ +DD+D S + ++ P APYWT P++MEKK
 Sbjct: 100 LCLARGSMIVLQNLTLITGDSSTSSNDEDEPKSHRDLNHRHSYPQQ-APYWTHPQRM 158
 Query: 74 LHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVP 133
 LHAVPA TVKF+CP++G P PT+RWLK+G+ F +RIGG ++R+ WS++M+SVVPSD
 Sbjct: 159 LHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGGNRIGGIRLRHQHNSLVMSVVP 218
 Query: 134 KGNVTCIVENEYGSINHTYQLDVVERSHPHPILOAGLPANKTVALGNSNVEFMCKVYSDPQ 193
 +G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +CKVYSD Q
 Sbjct: 219 RGTYTCLVENAVGSIRYNLLDVLERSPHRPILQAGLPANTTAVVGSVDVLLCKVYSDAQ 278

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Query: 194 PHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTLFNVTEAQSGEYVCKVSNY 253
          PHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GEY C N
Sbjct: 279 PHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGEYTCLAGNS 338

Query: 254 IGEANQSAWLTVTRPVAKALEERPAMVMTSPLYLEIIYCTGAPLISCMGLGSVIIYKMKSG 313
          IG + QSAWLTV P P + C + + ++SG
Sbjct: 339 IGLSYQSAWLTVL-----PGTGRIP-----HLTCDSLTPAGRTKSPTLQFSLESG 383

Query: 314 TKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSE 373
          + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNMVKIADF
Sbjct: 384 S-----SGKSSSS-----LVRGVRLSSSGPALLAGLVLS 411

Query: 374 YELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAAEIGLDDKDKPNRVTKVAVKMLKSDATE 433
          +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKMLK +A++
Sbjct: 412 LDLPDLPLWEFPRDRLVLGKPLGEGCFGQVVRAEA FGMDFARPDAQASTVAVKMLKDNASD 471

Query: 434 KDLSDLISEMEMMKMIGKHKNINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLE 493
          KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+ARRPPG +
Sbjct: 472 KDLADLVSEMEVMKLGIRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPD 531

Query: 494 YCYNPSHNPEEQLSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMVKIADF 553
          + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNMVKIADF
Sbjct: 532 LSPDGPSSSEGLSFFVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDNMVKIADF 591

Query: 554 GLARDIHHIDYKKTITNGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYP 613
          GLAR +HHIDYKKT+NGRLPVKWMapeALFDR+YTHQSDVWSFG+LLWEIFTLGGSPYP
Sbjct: 592 GLARGVHHIDYKKTISNGRLPVKWMapeALFDRVYTHQSDVWSFGILLWEIFTLGGSPYP 651

Query: 614 GVPVEELFKLLKEGHRMDKPSNCTNELYMMRDCWHAVPSQRPTFKQLVEVLDRIVALT 673
          G+PVEELF LL+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD+++ L
Sbjct: 652 GIPVEELFSLREGHRMDRPPHCPPELYGLMRECWAAPSQRPTEFKQLVEALDKVL-LAV 710

Query: 674 NQEYLDLSIPLDQYSPSPDTRSSSTCSSGEDSVFSHEPLP 713
          ++EYLDL + YSPS D SSTCSS DSVFSH+PLP
Sbjct: 711 SEEYLDLRLTFGPYSPSGGDA-SSTCSS-SDSVFSHDPLP 748

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tr Q8IXC7      Isoform of FGFR2 [FGFR2 AT-I] [Homo sapiens (Human)] 709 AA
Q8IXC7_HUMAN align

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Score = 770 bits (1989), Expect = 0.0
Identities = 420/753 (55%), Positives = 502/753 (66%), Gaps = 83/753 (11%)

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Query: 1 MWGWKCLFVAVLVATLCTARPAPTLPEQDALPSSSEDDDDSSSEKETDNTKPNPV 60
          M W + V+ ATL ARP+ +L E L E P
Sbjct: 1 MVSWGRFICLVVVMTATLSLARPSFSLVEDTTLEPE-----PP 39

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHR---IGGYKV 117
          Y S + +++ +++++ +C + W K+G P++R IG Y
Sbjct: 40 TKYQIS---QPEYVAAPGESLEVRCLLKDA--VISWTKDGVHLGPNRTVTLIGEY-- 91

Query: 118 RYATWSIIMDSVVPSSDKGNVTCIVENEYGSINHTYQLDVVE----- 158
          + + P D G Y C S + ++V +
Sbjct: 92 -----LQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145

Query: 159 -----RSPHRPILQAGLPANKTVALGNSVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPD 212
          R+P+ + V + V+F C +P P ++WLK NG + +
Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPMTMRWLK---NGKEFKQE 201

Query: 213 NLPYVQILKHSGINSSDAE-VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAK 271
          + + G + L + +V + G Y C V N G N + L V P
Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSSDKGNVTCIVENEYGSINHTYHLDVVAP--- 251

Query: 272 ALEERPAMVMTSPLYLEIIYCTGAPLISCMGLGSVIIYKMKSGTKKSDPHSQMAVHKLAKS 331
          + SP YLEI IYC G FLI+CM+ +VI+ +MK+ TKK DF SQ AVHKL K
Sbjct: 252 --GREKEITASPDYLEIAIYICIGVFLIACMVVTVILCRMKNNTTKKPDFSSQPAVHKLTKR 309

Query: 332 IPLRRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWELPRDRL 389
          IPLRRQVTVSA+SS+SMNS LVR +RLSS+ TPMLAGVSEYELPEDP+WE PRD+L
Sbjct: 310 IPLRRQVTVSAESSSSMNSNTPLVRITTRLSSSTADTPMLAGVSEYELPEDPKWEFFPRDKL 369

Query: 390 VLGKPLGEGCFGQVVLAAEIGLDDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMI 449
          LGKPLGEGCFGQVV+AEA+G+DKDKP VAVKMLK DATEKDLSDL+SEMEMMKMI
Sbjct: 370 TLGKPLGEGCFGQVVMMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEMEMMKMI 429

Query: 450 GKHKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPEEQLSK 509
          GKHKNIINLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEEQ++ K
Sbjct: 430 GKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEEQMTFK 489

Query: 510 DLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMVKIADFGGLARDIHHIDYKKT 569
          DLVSC YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMVKIADFGGLARDI++IDYKKT
Sbjct: 490 DLVSTYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDYKKT 549

Query: 570 NGRLPVKWMapeALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHR 629
          NGRLPVKWMapeALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLLKEGHR

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Sbjct: 550 NGRLPVKWMAPEALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLLKEGHR 609

Query: 630 MDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSP 689
MDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE LDRI+ LT+N+EYLDLS PL+QYSP

Sbjct: 610 MDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPLEQYSP 669

Query: 690 SFPDTRSSSTCSSGSDSVFSHEPLPEEPCLPRHP 722
S+PDTRSS CSSG+DSVFS +P+P EPCLP++P

Sbjct: 670 SYPDTRSS-CSSGSDSVFSPDPMPYEPCLPQYP 701

tr Q96KE5 Fibroblast growth factor receptor 4 variant [Homo sapiens (Human)] 592 AA
Q96KE5_HUMAN align

Score = 735 bits (1898), Expect = 0.0
Identities = 377/593 (63%), Positives = 452/593 (76%), Gaps = 20/593 (3%)

Query: 126 MDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVERSHPRPILQAGLPANKTVALGSNVEFM 185
M+SVVPSD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T +GS+VE +

Sbjct: 1 MESVVPSPDRGTYTCLVENAVGSIRYNYLLDLVLESPHRPILQAGLPANTTAVVGSDEVLL 60

Query: 186 CKVYSDQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSDDAEVLTLEFNVTQAQSGE 245
CKVYSD QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L NV+ +GE

Sbjct: 61 CKVYSDAQPHIQWLKHIVINGSSFGADGFPYVQVLKTADINSSEVEVLYLRNVSAEDAGE 120

Query: 246 YVCKVSNYIGEANQSAWLTVTRPVAKALEERP---AVMTSPLYLEIIYCTGAFLISCM 302
Y C N IG + QSAWLTV EE P A Y +II+Y +G+ ++ +L

Sbjct: 121 YTCLAGNSIGLSYQSAWLTVLP-----EEDPTWTAAPPEARYPDIIYASGSLALAVLL 174

Query: 303 GSVIIYKMKSGTKKSDFHSQ--MAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVLRPSRL 360
++ ++ G H + V KL++ PL RQ ++ + SS +S LVR RL

Sbjct: 175 ---LLARLYRQCALHGRHPRPPATVQKLSR-FPLARQFSLESGSSGKSSSS--LVRGVRL 228

Query: 361 SSSGTPLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVT 420
SSSG +LAG+ +LP DP WE PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ +

Sbjct: 229 SSSGPALLAGLVSLDPLDPLWEFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQAS 288

Query: 421 KVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNL 480
VAVKMLK +A++KDL+DL+SEME+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNL

Sbjct: 289 TVAVKMLKDNASDKDLADLVSEMEVMKLIGRHKNIIINLLGVCTQEGPLYVIVECAAKGNL 348

Query: 481 REYLQARRPPGLECYNPSHNFEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNV 540
RE+L+ARRPPG + + + E LS LVSCAYQVARGM+YL S+KCIHRDLAARNV

Sbjct: 349 REFLRARPPGPDLSPDGPRSSGPLSFPVLVSCAYQVARGMQYLESRKCIIHRDLAARNV 408

Query: 541 LVTEDNMVKIADFLGARDIHHIDYKKTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVL 600
LVTEDNMVKIADFLGAR +HHIDYKKT+NGRLPVKWMAPEALFDR+YTHQSDVWSFG+L

Sbjct: 409 LVTEDNMVKIADFLARGVHHIDYKKTNGRLPVKWMAPEALFDRVYTHQSDVWSFGIL 468

Query: 601 LWEIFTLGGSPYPGPVVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQ 660
LWEIFTLGGSPYPG+PVEELF LL+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQ

Sbjct: 469 LWEIFTLGGSPYPGIPVEELFSLLECHHRMDRPPHCPPELYGLMRECWAAPSQRPTFKQ 528

Query: 661 LVEVLDRIVALTSNQEYLDLSIPLDQYSPSFPDTRSSSTCSSGSDSVFSHEPLP 713
LVE LD+++ L ++EYLDL + YSPS D SSTCSS DSVFSH+PLP

Sbjct: 529 LVEALDKVL-LAVSEYLDLRLTFGPYSPSGDA-SSTCSS-SDSVFSHDPLP 578

sp_vs P21802-15 Isoform 15 of P21802 - Homo sapiens (Human) [FGFR2] [Homo sapiens 705 AA
FGFR2_HUMAN (Human)] align

Score = 685 bits (1768), Expect = 0.0
Identities = 390/758 (51%), Positives = 480/758 (63%), Gaps = 97/758 (12%)

Query: 1 MWGWKCLFWAVLVTATLCTARPAPTLPBQDALPSSDDDDDDSSSEKETDNTKPNPV 60
M W + V+ ATL ARP+ +L E L E P

Sbjct: 1 MVSWGRFICLVVVVMTLSLARPSFSLVEDTTLEPEE-----PP 39

Query: 61 APYWTSPKMEKKLHAVPAAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHR---IGGYKV 117
Y S + +++ +++++ +C + W K+G P++R IG Y

Sbjct: 40 TKQKIS---QPEVYVAAPGESLEVRCLLKDA--VISWTKDGVHLGPNNRTVLIGEY-- 91

Query: 118 RYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQLDVVE----- 158
+ + P D G Y C S + ++V +

Sbjct: 92 -----LQIKGATPRDSGLYACTASRTVDSETWYFMVNVTDAISSGDEDDTDGAEDFVS 145

Query: 159 -----RSPHRPILQAGLPANKTVALGSNVEFMCKVYSDQPHIQWLKHIEVNGSKIGPD 212
R+P+ + V + V+F C +P P ++WLK NG + +

Sbjct: 146 ENSNNKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPMTMRWLK----NGKEFKQE 201

Query: 213 NLPYVQILKHSGINSDDAE-VLTLEFNVTQAQSGEYVCKVSNYIGEANQSAWLTVT----- 266

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      +      + G      +      L + +V + G Y C V N G N + L V
Sbjct: 202 H-----RIGGYKVRNQHWSLIMESVVPSPDKGNYTCVVENEYGSINHTYHLDVVERSPH 254
Query: 267 RPKAKALEERPAVMTSPPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHSQMAVH 326
      RP+ +A      PA ++ + ++      C + +      I +      K+G+K
Sbjct: 255 RPILQA--GLPANASTVVGDDVEFVCK--VYSDAQPHIQWIKHVEKNGSKYGP----- 303
Query: 327 KLAKSIPLRQVTVSADSSASMNSGVLLVR-PSRLSSSG-TPMLAGVSEYELPEDPRWEL 384
      +P + + VSA+SS+SMNS      LVR +RLSS+      TPMLAGVSEYELPEDP+WE
Sbjct: 304 ---DGLPYLKVLKVSAESSSSMNSNTPLVRIITRLSSTADTPMLAGVSEYELPEDPKWEF 360
Query: 385 PRDRLVLGKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEME 444
      PRD+L      LGKPLGEGCFGQVV+AEA+G+DKDKP      VAVKMLK      DATEKDLSDL+SEME
Sbjct: 361 PRDKLTLGKPLGEGCFGQVMAEAVGIDKDKPKEAVTVAVKMLKDDATEKDLSDLVSEME 420
Query: 445 MMKMIGKHKNI INLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPPEE 504
      MMKMIGKHKNI INLL ACTQDGPLYVIVEYASKGNLREYL+ARRPPG+EY Y+ + PEE
Sbjct: 421 MMKMIGKHKNI INLLGACTQDGPLYVIVEYASKGNLREYLARRPPGMEYSYDINRVPEE 480
Query: 505 QLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDY 564
      Q++      KDLVSC      YQ+ARGMEYLAS+KCIHRDLAARNVLVTE+NMKIADFGGLARDI++IDY
Sbjct: 481 QMTFKDLVSCITYQLARGMEYLASQKCIHRDLAARNVLVTENNVMKIADFGGLARDINNIDY 540
Query: 565 YKKTNGRLPVKWMAPALFDRITYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLL 624
      YKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVL+WEIFTLGGSPYPG+PVEELFKLL
Sbjct: 541 YKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLMWEIFTLGGSPYPGIPVEELFKLL 600
Query: 625 KEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPL 684
      KEGHRMDKP+NCTNELYMMMRDCWHAVPSQRPTFKQLVE      LDRI+      LT+N+EYLDLS      PL
Sbjct: 601 KEGHRMDKPANCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRILTLTNEEYLDLSQPL 660
Query: 685 DQYSPSPDTRSSSCSSGEDSVFSHEPLPEEPCLPHP 722
      +QYSPS+PDTRSS      CSSG+DSVFS +P+P      EPCLP++P
Sbjct: 661 EQYSPSPDTRSS--CSSGDDSVFSPDPMPYEPCLPQYP 697

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tr Q59FL9      Fibroblast growth factor receptor 3 isoform 1 variant (Fragment) 879 AA
Q59FL9_HUMAN  [Homo sapiens (Human)] align

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Score = 684 bits (1764), Expect = 0.0
 Identities = 346/539 (64%), Positives = 421/539 (78%), Gaps = 15/539 (2%)

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Query: 34 PSSDDDDDDSSSEKETDNTKPNFVAPYWTSPPEKMEKHLHAVPAAKTVKFKCPSSGTP 93
      PSS DD+D +D      E ++T +      APYWT PE+M+KKL AVPA      TV+F+CP++G P
Sbjct: 216 PSSDDDDGED-----EAEDTGVDTGAPYWTRPERMDKLLAVPAANTVRFRCPAAGNP 269
Query: 94 NPTLRWLKNGKEBPKPDHRIGGYKVRYATWSIIMDSVVPSPDKGNYTCIVENEYGSINHTYQ 153
      P++      WLKNG+EF+ +HRIGG K+R+      WS++M+SVVPSD+GNYTC+VEN++GSI      TY
Sbjct: 270 TPSILWLNKNGREFRGEHRIGGKLRHQQVSLVMSVVPSPDRGNYTCVENKFGSIRQTYT 329
Query: 154 LDVVERSHPRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
      LDV+ERSHPRPILQAGLPAN+T      LGS+VEF      CKVYSD      QPHIQWLKH+EVNGSK+GPD
Sbjct: 330 LDVLEERSHPRPILQAGLPANQTAVLGSDFEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDPG 389
Query: 214 LPYVQILKHSGINSDDAE--VLTLFNVTEAQSGEYVCKVSNYIGEANQSAWLTVTRPVAK 271
      PYV +LK +G N++D E      VL+L NVT      +GEY C      N IG ++      SAWL V      P +
Sbjct: 390 TPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFHHSAWLVVL-PAEE 448
Query: 272 ALEERPAVMTSPPLYLEIIYCTGAFLISCMGLGSVIIYKMKSGTKKSDFHSQMAVHLAKS 331
      L E A      +Y I+ Y G FL      ++ +V + ++S      KK      VHK+++
Sbjct: 449 ELVE--ADEAGSVYAGILSYGVGFLLFILVVAAVTLCRLRSPPKG--LGSPTVHKISR- 503
Query: 332 IPLRRQVTVSADSSASMNSGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVL 391
      PL+RQ      VS +S+ASM+S      LVR +RLSS      P LA VSE      ELP DP+WEL R      RL L
Sbjct: 504 FPLKRQ-QVSLASNAMSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTL 562
Query: 392 GKPLGEGCFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGK 451
      GKPLGEGCFGQVV+AEAIG+DKD+      +      VAVKMLK      DAT+KDLSDL+SEMEMMKMIGK
Sbjct: 563 GKPLGEGCFGQVMAEAGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGK 622
Query: 452 HKNIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNPPEEQLSKDL 511
      HKNIINLL ACTQ      GPLYV+VEYA+KGNLRE+L+ARRPPGL+Y ++      PEEQL+      KDL
Sbjct: 623 HKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCPPPEQLTFKDL 682
Query: 512 VSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNMKIADFGGLARDIHHIDYKKTN 570
      VSCAYQVARGMEYLAS+KCIHRDLAARNVLVTEDNMKIADFGGLARD+H++DYKKTN
Sbjct: 683 VSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNMKIADFGGLARDVHNLDYKKTN 741

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tr A8E633      Putative uncharacterized protein (Fragment) [Homo sapiens (Human)] 480 AA
A8E633_HUMAN align

```

Score = 646 bits (1667), Expect = 0.0
Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

```

Query: 243 SGEYVCKVSNYIGEANSQSAWLTVTTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFILISCM 302
+GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++
Sbjct: 8 AGEYTCAGNSIGFSSHSWLVVL-PAEEELVE--ADEAGSVYAGILSYGVGFLLFVLV 64

Query: 303 GSVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362
+V + +++S KK VHK+++ PL+RQV S +S+ASM+S LVR +RLSS
Sbjct: 65 AAVTLCRLRSPPKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKV 422
P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVV+AEAIG+DKD+ + V
Sbjct: 120 GEGPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVVMAEAGIDKDRRAKPVTV 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPVYVIVEYASKGNLRE 482
AVKMLK DAT+KDLSDL+SEMEMMKMIGKHKNIINLL ACTQ GPLYV+VEYA+KGNLRE
Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVVLVEYAAKGNLRE 239

Query: 483 YLQARRPPGLECYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLV 542
+L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+KCIHRDLAARNVLV
Sbjct: 240 FLRARRPPGLDYSPDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLV 299

Query: 543 TEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLW 602
TEDNVMKIADFGLARD+H++DYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVLLW
Sbjct: 300 TEDNVMKIADFGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLLW 359

Query: 603 EIPTLGGSPYPGVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662
EIPTLGGSPYPG+PVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWAH PSQRPTFKQLV
Sbjct: 360 EIPTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWAHAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTNSQEYLDLSIPLDQYSPSPFDTRSSSCSGEDSVFSHEPLPEEP 716
E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P
Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS--SSGDDSVFAHDLLEPPAP 472

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tr Q0IJ44 FGFR3 protein (Fragment) [FGFR3] [Homo sapiens (Human)] 480 AA
Q0IJ44_HUMAN align

Score = 646 bits (1666), Expect = 0.0
Identities = 328/474 (69%), Positives = 383/474 (80%), Gaps = 9/474 (1%)

```

Query: 243 SGEYVCKVSNYIGEANSQSAWLTVTTRPVAKALEERPAVMTSPLYLEIIIIYCTGAFILISCM 302
+GEY C N IG ++ SAWL V P + L E A +Y I+ Y G FL ++
Sbjct: 8 AGEYTCAGNSIGFSSHSWLVVL-PAEEELVE--ADEAGSVYAGILSYGVGFLLFVLV 64

Query: 303 GSVIIYKMKSGTKKSDPHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGVLLVRPSRLSS 362
+V + +++S KK VHK+++ PL+RQV S +S+ASM+S LVR +RLSS
Sbjct: 65 AAVTLCRLRSPPKKG--LGSPTVHKISR-FPLKRQV--SLESNASMSSNTPLVRIARLSS 119

Query: 363 SGTPLMAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAGLDKDKPNRVTKV 422
P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVV+AEAIG+DKD+ + V
Sbjct: 120 GEGPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVVMAEAGIDKDRRAKPVTV 179

Query: 423 AVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLEACTQDGPVYVIVEYASKGNLRE 482
AVKMLK DAT+KDLSDL+SEMEMMKMIGKHKNIINLL ACTQ GPLYV+VEYA+KGNLRE
Sbjct: 180 AVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVVLVEYAAKGNLRE 239

Query: 483 YLQARRPPGLECYNPSHNPEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLV 542
+L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+KCIHRDLAARNVLV
Sbjct: 240 FLRARRPPGLDYSPDTCKPPEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLV 299

Query: 543 TEDNVMKIADFGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYTHQSDVWSFGVLLW 602
TEDNVMKIADFGLARD+H++DYKKTNGRLPVKWMAPALFDR+YTHQSDVWSFGVLLW
Sbjct: 300 TEDNVMKIADFGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYTHQSDVWSFGVLLW 359

Query: 603 EIPTLGGSPYPGVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLV 662
EIPTLGGSPYPG+PVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWAH PSQRPTFKQLV
Sbjct: 360 EIPTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWAHAPSQRPTFKQLV 419

Query: 663 EVLDRIVALTNSQEYLDLSIPLDQYSPSPFDTRSSSCSGEDSVFSHEPLPEEP 716
E LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H+ LP P
Sbjct: 420 EDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSS--SSGDDSVFAHDLLEPPAP 472

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sp_vs P22607-3 Isoform 3 of P22607 - Homo sapiens (Human) [FGFR3] [Homo sapiens 694 AA
FGFR3_HUMAN (Human)] align

Score = 625 bits (1611), Expect = e-178
 Identities = 332/547 (60%), Positives = 393/547 (71%), Gaps = 32/547 (5%)

Query: 176 VALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTL 235
 V + V F C + P P I WLK NG + ++ L+H + L +
 Sbjct: 166 VPAANTVRFRCPAAGNPTPSISWLK---NGREFRGEHRIGGIKLRHQQS-----LVM 215

Query: 236 FNVTEAQSGEYVCKVSNYIGEANQSAWLTVT----RPVAKALEERPAVMTSPLYLEIII 290
 +V + G Y C V N G Q+ L V RP+ +A PA T+ L ++
 Sbjct: 216 ESVPSPDRGNYTCVVENKFGSIRQTYTLDVLESPHRPILQA--GLPANQTAVLGSDVEF 273

Query: 291 YCTGAFLISCMLGSVIIYKMKSGTKKSDPHSQMAVHKLAKE-IPLRRQVTVSADSSASMN 349
 +C +Y + H ++ K+ P + VS +S+ASM+
 Sbjct: 274 HCK-----VYSDAQPHIQWLKHVEVNGSKVGPDPGTPYVTVLKVSLASNAMS 320

Query: 350 SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGCFGQVVLAEAI 409
 S LVR +RLSS P LA VSE ELP DP+WEL R RL LGKPLGEGCFGQVVAEAI
 Sbjct: 321 SNTPLVRIARLSSSGEPTLANVSELELPADPKWELSRARLTGKPLGEGCFGQVMAEAI 380

Query: 410 GLDKDKPNRVTKVAVKMLKSDATEKDLSLISEMEMMKMIGKHKNIIINLLEACTQDGPLY 469
 G+DKD+ + VAVKMLK DAT+KDLSDL+SEMEMMKMIGKHKNIIINLL ACTQ GPLY
 Sbjct: 381 GIDKDRAAKFPVTAVKMLKDDATDKDLSLISEMEMMKMIGKHKNIIINLLGACTQGGPLY 440

Query: 470 VIVEYASKGNLREYLQARRPPGLECYNPSHNPPEEQLSKDLVSCAYQVARGMEYLASKK 529
 V+VEYA+KGNLRE+L+ARRPPGL+Y ++ PEEQL+ KDLVSCAYQVARGMEYLAS+K
 Sbjct: 441 VLVEYAAKGNLREPLRARRPPGLDYSFDTCKPPEEQLTFLDLVSCAYQVARGMEYLASQK 500

Query: 530 CIHRDLAARNVLVTEDNMVKIADFGGLARDIHHIDYKKTNGRLPVKWMAPALFDRIYT 589
 CIHRDLAARNVLVTEDNMVKIADFGGLARD+H++DYKKTNGRLPVKWMAPALFDR+YT
 Sbjct: 501 CIHRDLAARNVLVTEDNMVKIADFGGLARDVHNLDDYKKTNGRLPVKWMAPALFDRVYT 560

Query: 590 HQSDVWSFGVLLWEIFTLGGSPYPGPVPEELFKLLKEGHRMDKPSNCTNELYMMMRDCWH 649
 HQSDVWSFGVLLWEIFTLGGSPYPGP+PVEELFKLLKEGHRMDKP+NCT++LYM+MR+CWH
 Sbjct: 561 HQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWH 620

Query: 650 AVPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIPLDQYSPSPDTRSSSTCSSGDSVFSH 709
 A PSQRPTFKQLVE LDR++ +TS EYLDLS P +QYSP DT SS+ SSG+DSVF+H
 Sbjct: 621 AAPSQRPFTFKQLVEDLDRVLTSTDEYLDLSAPFQYSPGGQDTPSSS--SSGDSVFAH 679

Query: 710 EPLPEEP 716
 + LP P
 Sbjct: 680 DLLPPAP 686

Score = 280 bits (717), Expect = 5e-75
 Identities = 131/213 (61%), Positives = 165/213 (77%), Gaps = 7/213 (3%)

Query: 34 PSSDDDDDDSSSEEEKETDNTKPNPVAPYWTSPKMEKKLHAVPAAKTVKPKCPSSGTP 93
 PSS DD+D +D E ++T + APYWT PE+M+KKL AVPAA TV+F+CP++G P
 Sbjct: 129 PSSDDEDEDG-----EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNP 182

Query: 94 NPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPDKGNYTCIVENEYGSINHTYQ 153
 P++ WLKNG+EF+ +HRIGG K+R+ WS++M+SVVPSD+GNYTC+VEN++GSI TY
 Sbjct: 183 TPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMSVVPSPDRGNYTCVVENKFGSIRQTYT 242

Query: 154 LDVVERSPhRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDN 213
 LDV+ERSPhRPILQAGLPAN+T LGS+VEF CKVYSD QPHIQWLKH+EVNGSK+GPD
 Sbjct: 243 LDVLESPHRRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHIEVNGSKVGPDG 302

Query: 214 LPYVQILKHS-GINSSDAEVLTLFNVTEAQSGE 245
 PYV +LK S N+S + L + SGE
 Sbjct: 303 TPYVTVLKVSLASNASSSNTPLVRIARLSSGE 335

tr Q59F30 Fibroblast growth factor receptor 4 variant (Fragment) [Homo sapiens 1034 AA
 Q59F30_HUMAN (Human)] align

Score = 553 bits (1426), Expect = e-157
 Identities = 285/450 (63%), Positives = 348/450 (77%), Gaps = 13/450 (2%)

Query: 268 PVAKALEERPAVMTSP--LYLEIIIIYCTGAPLISCMLGSVIIYKMKSGTKKSDPHSQ--M 323
 P A+A E+ +P Y +II+Y +G+ ++ +L ++ ++ G H +
 Sbjct: 580 PCARAEEDPTWTAAPAEARYTDIILYASGSLALAVLL---LLARLYRGQALHGRHPRPPA 636

Query: 324 AVHKLAKSIPLRRQVTVSADSSASMN SGVLLVRPSRLSSSGTPMLAGVSEYELPEDPRWE 383
 V KL++ PL RQ ++ + SS +S LVR RLSSSG +LAG+ +LP DP WE
 Sbjct: 637 TVQKLSR-FPLARQFSLES GSGSKSSS--LVRGVRLSSSGPALLAGLVSLDPLDPLWE 693

Query: 384 LPRDRLVLGKPLGEGCFGQVVLAEAIAGLDKDKPNRVTKVAVKMLKSDATEKDLSLISEM 443
 PRDRLVLGKPLGEGCFGQVV AEA G+D +P++ + VAVKMLK +A++KDL+DL+SEM
 Sbjct: 694 FPRDRLVLGKPLGEGCFGQVVAEAFGMDPARPDQASTVAVKMLKDNASDKDLADLVSEM 753

Query: 444 EMMKMIGKHKNIIINLLEACTQDGPLYVIVEYASKGNLREYLQARRPPGLECYNPSHNP 503
 E+MK+IG+HKNIINLL CTQ+GPLYVIVE A+KGNLRE+L+ARRPPG + + + E

Sbjct: 754 EVMKLIGRHNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARRPPGPDLSPDGPRSS 813

Query: 504 EQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGGLARDIHIIID 563
 LS LVSCAYQVARGM+YL S+KCIHRDLAARNVLVTEDNVMKIADFGGLAR +HHID

Sbjct: 814 GPLSPFVLVSCAYQVARGMQYLESRKCIHRDLAARNVLVTEDNVMKIADFGGLARGVHHID 873

Query: 564 YYKKTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKL 623
 YYKKT+NGRLPVKWMAPEALFDR+YTHQSDVWSFG+LLWEIFTLGGSPYPG+PVEELF L

Sbjct: 874 YYKKTNGRLPVKWMAPEALFDRVYTHQSDVWSFGILLWEIFTLGGSPYPGIPVEELFSL 933

Query: 624 LKEGHRMDKPSNCTNELYMMRDWCWHA VPSQRPTFKQLVEVLDRIVALTSNQEYLDLSIP 683
 L+EGHRMD+P +C ELY +MR+CWHA PSQRPTFKQLVE LD+++ L ++EYLDL +

Sbjct: 934 LREGHRMDRPPHCPPELYGLMRECWHAAAPSQRPTFKQLVEALDKVL-LAVSEEYLDLRLT 992

Query: 684 LDQYSPSPDPTRSSSTCSSGSDSVFSHEPLP 713
 YSPS D SSTCSS DSVFSH+PLP

Sbjct: 993 FGPYSPSGDA-SSTCSS-SDSVFSHDPLP 1020

Score = 295 bits (754), Expect = 2e-79
 Identities = 134/209 (64%), Positives = 164/209 (78%)

Query: 57 PNPVAPYWTSPKMEKKLHAVPAKTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYK 116
 P P APYWT P++MEKKLHAVPA TVKF+CP++G P PT+RWLK+G+ F ++RIGG +

Sbjct: 257 PCPPAPYWTHPQRMEKKLHAVPAGNTVKFRCPAAGNPTPTIRWLKDGQAFHGENRIGGIR 316

Query: 117 VRYATWSIIIMDSVPSDKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQAGLPANKTV 176
 +R+ WS++M+SVVPSD+G YTC+VEN GSI + Y LDV+ERSPHRPILQAGLPAN T

Sbjct: 317 LRHQHWSLVMSVSPSDRGTYTCLVENAVGSIIRYNYLLDVLESPHRPILQAGLPANTTA 376

Query: 177 ALGSNVEFMCKVYSDFPHIQWLKHIEVNGSKIGPDNLPYVQILKHSGINSSDAEVLTLF 236
 +GS+VE +CKVYSD QPHIQWLKHI +NGS G D PYVQ+LK + INSS+ EVL L

Sbjct: 377 VVGSDEVLLCKVYSDAQPHIQWLKHIVINGSSFGADGFFVQVLKTADINSSEVEVLYLR 436

Query: 237 NVTEAQSGEYVCKVSNYIGEANQSAWLTV 265
 NV+ +GEY C N IG + QSAWLTV

Sbjct: 437 NVSAEDAGEYTCLAGNSIGLSYQSAWLTV 465

Subset of the database(s) listed below
 Number of letters searched: 35,064,127
 Number of sequences searched: 82,088

Database: UniProtKB Homo sapiens
 Posted date: Nov 12, 2007 6:33 PM
 Number of letters in database: 25,263,043
 Number of sequences in database: 64,426

Database: UniProtKB_HUMAN.01
 Posted date: Nov 12, 2007 6:36 PM
 Number of letters in database: 9,801,084
 Number of sequences in database: 17,662

Lambda	K	H
0.316	0.133	0.405

Gapped Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 59,077,092
 Number of Sequences: 2526181
 Number of extensions: 2919052
 Number of successful extensions: 26662
 Number of sequences better than 10.0: 1000
 Number of HSP's better than 10.0 without gapping: 1277
 Number of HSP's successfully gapped in prelim test: 935
 Number of HSP's that attempted gapping in prelim test: 15141
 Number of HSP's gapped (non-prelim): 6214
 length of query: 733
 length of database: 35,064,127
 effective HSP length: 114
 effective length of query: 619
 effective length of database: 25,706,095
 effective search space: 15912072805
 effective search space used: 15912072805
 T: 11
 A: 40
 X1: 16 (7.3 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.6 bits)
 S2: 68 (30.8 bits)
 Wallclock time: 4 seconds

